



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ashkenazi et al.) Group Art Unit Unknown
Appl. No. : 10/017,086)
Filed : October 24, 2001) I hereby certify that this correspondence and all
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Examiner : Unknown)
April 25, 2002
(Date)
Ginger R. Dreger, Reg. No. 33,055

SEQUENCE SUBMISSION STATEMENT

Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, mailed April 2, 2002. I hereby state that the amendments, made in accordance with 37 C.F.R. § 1.825(a) and included in the Substitute Sequence Listing submitted herewith, are supported in the application, and that the Substitute Sequence Listing does not include new matter.

I further state that the information recorded in the currently submitted substitute copy of the computer-readable form of the Sequence Listing is identical to the paper form of the Sequence Listing submitted herewith as required in 37 C.F.R. § 1.825(b).

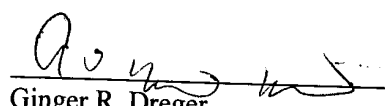
Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: April 25, 2002

By:


Ginger R. Dreger
Registration No. 33,055
Attorney of Record
620 Newport Center Drive, 16th Floor
Newport Beach, CA 92660
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#5

Sequence Listing

<110> Ashkenazi, Avi
Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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cagggtttttt cctttaaaaa aattatagac acggttcact aaattgattt 2800
 agtcagaatt cctagactga aagaacctaa acaaaaaaat atttttaaaga 2850
 tataaatata tgctgtatat gttatgtaat ttatttttagg ctataataca 2900
 tttcctatttt tcgcattttc aataaaatgt ctctaataca aaaaa 2945

<210> 7
 <211> 492
 <212> PRT
 <213> Homo sapiens

<400> 7
 Met Val Lys Phe Pro Ala Leu Thr His Tyr Trp Pro Leu Ile Arg
 1 5 10 15
 Phe Leu Val Pro Leu Gly Ile Thr Asn Ile Ala Ile Asp Phe Gly
 20 25 30
 Glu Gln Ala Leu Asn Arg Gly Ile Ala Ala Val Lys Glu Asp Ala
 35 40 45
 Val Glu Met Leu Ala Ser Tyr Gly Leu Ala Tyr Ser Leu Met Lys
 50 55 60
 Phe Phe Thr Gly Pro Met Ser Asp Phe Lys Asn Val Gly Leu Val
 65 70 75
 Phe Val Asn Ser Lys Arg Asp Arg Thr Lys Ala Val Leu Cys Met
 80 85 90

Val Val Ala Gly Ala Ile Ala Ala Val Phe His Thr Leu Ile Ala
 95 100 105
 Tyr Ser Asp Leu Gly Tyr Tyr Ile Ile Asn Lys Leu His His Val
 110 115 120
 Asp Glu Ser Val Gly Ser Lys Thr Arg Arg Ala Phe Leu Tyr Leu
 125 130 135
 Ala Ala Phe Pro Phe Met Asp Ala Met Ala Trp Thr His Ala Gly
 140 145 150
 Ile Leu Leu Lys His Lys Tyr Ser Phe Leu Val Gly Cys Ala Ser
 155 160 165
 Ile Ser Asp Val Ile Ala Gln Val Val Phe Val Ala Ile Leu Leu
 170 175 180
 His Ser His Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu
 185 190 195
 Ser Leu Tyr Met Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu
 200 205 210

Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly	215	220	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
<hr/>			
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tgagcttctg gtgccntttg gctctaattc tggccacaca gagaancagt 100
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
ggccacatc aagaagtcca ccttcgtctg catggctctg tcactcacgc 350
tctgtttcgt gatgttttgg acaccaacg tgtctngaa aatcttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggctggg tatcctgggt tngacaagat aaacccccag 50
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150
gttttgga cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200
tggantttgc ctttgagaa ntttgngntg ttcctttgcg gattttctcc 250
tttttccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattcccagt tccggtcacg gggagggcgc atntcacggg gtggctgang 50
aactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100
cgctctcatc gccagcctng tggtcctacc ctacctgggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattcttcc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgccca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50
gcctgcctgg gagcctgtc cctgctcagc tgcggtcct gcctctgcgg 100
ctctgcccc tgcactctgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
ttaagttcct gatcctggtg ggctcaccg tgggtgcctt ctacatccct 500
gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550
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ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650
tacgcaggcc tcttcttctt cactctctc ttctacttgc tgctgatcgc 700
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
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atcgtgctg tcctgccaa ggtccaggac gccagccca actcgggtct 850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950
ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000

gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc 1050
tcttcatcag tctgcgtcc tcagaccacc ggcaggtgaa cagcctgatg 1100
cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150
gcaggtgga gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
tcacctacag ctactcctt ttccattct gcctgggtgct ggctcactg 1250
cacgtcatga tgacgtcac caactggtac aagcccgtg agaccggaa 1300
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
cagggtgct cctctacctg tggacctgg tagcccaact cctcctgcgc 1400
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgccctc 1450
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caccaatcag ccaggctgag cccccacccc tgcccagct ccaggacctg 1550
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caggctcctg cagagcccca tcccccgcc acaccacac ggtggagctg 1650
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 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc cccagggga cctgcccc ttctggact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
 1 5 10 15
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20 25 30
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35 40 45
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50 55 60

Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
 65 70 75
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
 80 85 90
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
 95 100 105
 Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
 110 115 120
 Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe
 125 130 135
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
 140 145 150
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
 155 160 165
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
 170 175 180

Asp	Phe	Ala	His	Ser 185	Trp	Asn	Gln	Arg	Trp 190	Leu	Gly	Lys	Ala	Glu 195
Glu	Cys	Asp	Ser	Arg 200	Ala	Trp	Tyr	Ala	Gly 205	Leu	Phe	Phe	Phe	Thr 210
Leu	Leu	Phe	Tyr	Leu 215	Leu	Ser	Ile	Ala	Ala 220	Val	Ala	Leu	Met	Phe 225
Met	Tyr	Tyr	Thr	Glu 230	Pro	Ser	Gly	Cys	His 235	Glu	Gly	Lys	Val	Phe 240
Ile	Ser	Leu	Asn	Leu 245	Thr	Phe	Cys	Val	Cys 250	Val	Ser	Ile	Ala	Ala 255
Val	Leu	Pro	Lys	Val 260	Gln	Asp	Ala	Gln	Pro 265	Asn	Ser	Gly	Leu	Leu 270
Gln	Ala	Ser	Val	Ile 275	Thr	Leu	Tyr	Thr	Met 280	Phe	Val	Thr	Trp	Ser 285
Ala	Leu	Ser	Ser	Ile 290	Pro	Glu	Gln	Lys	Cys 295	Asn	Pro	His	Leu	Pro 300
Thr	Gln	Leu	Gly	Asn 305	Glu	Thr	Val	Val	Ala 310	Gly	Pro	Glu	Gly	Tyr 315
Glu	Thr	Gln	Trp	Trp 320	Asp	Ala	Pro	Ser	Ile 325	Val	Gly	Leu	Ile	Ile 330
Phe	Leu	Leu	Cys	Thr 335	Leu	Phe	Ile	Ser	Leu 340	Arg	Ser	Ser	Asp	His 345
Arg	Gln	Val	Asn	Ser 350	Leu	Met	Gln	Thr	Glu 355	Glu	Cys	Pro	Pro	Met 360
Leu	Asp	Ala	Thr	Gln 365	Gln	Gln	Gln	Gln	Gln 370	Val	Ala	Ala	Cys	Glu 375
Gly	Arg	Ala	Phe	Asp 380	Asn	Glu	Gln	Asp	Gly 385	Val	Thr	Tyr	Ser	Tyr 390
Ser	Phe	Phe	His	Phe 395	Cys	Leu	Val	Leu	Ala 400	Ser	Leu	His	Val	Met 405
Met	Thr	Leu	Thr	Asn 410	Trp	Tyr	Lys	Pro	Gly 415	Glu	Thr	Arg	Lys	Met 420
Ile	Ser	Thr	Trp	Thr 425	Ala	Val	Trp	Val	Lys 430	Ile	Cys	Ala	Ser	Trp 435
Ala	Gly	Leu	Leu	Leu 440	Tyr	Leu	Trp	Thr	Leu 445	Val	Ala	Pro	Leu	Leu 450
Leu	Arg	Asn	Arg	Asp 455	Phe	Ser								

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcatccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
cttcttccac ttctgcttg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcaccc acgg 24

<210> 25
<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

tggcacagat cttcaccac acgg 24

<210> 26

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27

<211> 1351

<212> DNA

<213> Homo sapiens

<400> 27

gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50

ttaacctggg tcaaatgcac ggattctcac ctcgtagagt tacgtctctc 100

cgcggcacgt ccgcgaggac ttgaagtccg gagcgctcaa gtttgtccgt 150

aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200

tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300

cccagagccc tattaccgg aatctggatg ggaccgctc cgggagctgt 350

ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400

aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450

agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500

tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550

cgaggcttca ttcgttatgg ctggcgctgg ggttgagaa ctgcagtgtt 600

tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650

aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt 700

tttaggataa acgtaggcct gcgtggcctg gtggctgggtg gcataattgg 750

agccttgctg ggcaactcctg taggaggcct gctgatggca tttcagaagt 800

acgctgggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900
 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
 atgctaagaa aattgaagca ctgctaaacc ttctagaaa cccttcagta 1000
 atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050
 gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100
 tctttggtca gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150
 tggcttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200
 gtactctcac ttactttatc cttaaattta aatacatact tatgtttgta 1250
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
 t 1351

<210> 28
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 28

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala
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Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20					25					30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val
				35					40					45

Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu
				50					55					60

Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala
				65					70					75

Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val
				80					85					90

Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile
				95					100					105

Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val
				110					115					120

Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly
				125					130					135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn
				140					145					150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu
				155					160					165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg
				170					175					180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly
				185					190					195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln
				200					205					210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg
				215					220					225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu
				230					235					240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg
				245					250					255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu
				260					265					270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp
				275					280					285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50

ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200

catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250

ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300

ttcgttcattg gctggcgccg aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50
accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
gcggttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcattcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgccgc cgcgcgcgcg ccgcgcactg cagccccagg ccccggcccc 50

ccaccacagt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100

gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150

tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250

gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300

tccgagtggc cggcgtggtc attgcagtgg gcatcttctt gttcctgatt 350

gcttttagtg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400

tttttatatg attattctgt tacttgtatt tattgttcag ttttctgtat 450

cttgcgcttg ttagccctg aaccaggagc aacaggggtca gcttctggag 500

gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550

aaactgctgt gggttccgaa gtgttaaccc aaatgacacc tgtctggcta 600

gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650

gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750

agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800

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cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

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 atctcccata atttgaaatt gaaatcgat tgtgtggctc tgtatattct 1750
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 taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile	30
				20					25						
Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val	45
				35					40						
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	60
				50					55						
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	75
				65					70						
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	90
				80					85						
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	105
				95					100						

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn
 110 115 120
 Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn
 125 130 135
 Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser
 140 145 150
 Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val
 155 160 165
 Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu
 170 175 180
 Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp
 185 190 195
 Pro Arg Ala Asn Pro Ser Ala Phe Leu
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<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300
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 gatcctgggt gtttggtga cctacagata caggaaccag 390

<210> 38
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttgnctt tttagggaaa gatgtgtgt 50
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ttacaccaat gtattctaga atagttatgt cttaggaaat tgtgggttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
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taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgttttagc ccctgaaacc aggagcaaca gggncagct tcctggaggt 100
tggttggtgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taaccctaat gacacctgtc 200
tggtctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40
accacgtct gcgttgctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ggccccaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
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gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400
cgtggtacaa aaggcagaca gcgggcacta cactgcagt ggcatcttcc 450
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gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550
acccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600
tgcagaggtc agctgccgc ctctcttct cttctacaa ggatggaagg 650
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agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750
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cctcatctgt atcaccagat gggccttctt ctcaaacaca tgcaggatgt 1000
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 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccctt 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctgggtgt 2050
 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
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 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75

Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val
 155 160 165
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala
 170 175 180
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 46
 tgggctgtgt cctcatgg 18

<210> 47
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 47
 tttccagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgcccacg ggtccgcca cgcgtccggg 50
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 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75

His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
 185 190 195

Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe
 200 205 210
 Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile
 215 220 225
 Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
 230 235 240
 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser
 245 250 255
 Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr
 260 265 270
 Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe
 275 280 285
 Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr
 290 295 300
 Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His
 305 310 315
 Val Tyr Glu Ala Ala Arg
 320

<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tatccctcca attgagcacc ctgg 24

<210> 54

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 54

gtcgggaagac atcccaacaa g 21

<210> 55

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55
cttcacaatg tcgctgtgct gctc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
agccaaatcc agcagctggc ttac 24

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58
<211> 2458
<212> DNA
<213> Homo sapiens

<400> 58
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cgccccgcac atggctgcag ccacctcgcg cgcaccccga ggccgcccgc 100
ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150
agcaactgag cggggaagcg cccgcgtccg gggatcgga tgcctcct 200
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caaagcagaa accacaccca gcatgatccc cagccagagc agagccttcc 1300
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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
				20					25					30

Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45

Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60

Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75

Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
				80					85					90

Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105

Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120

Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135

Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140					145					150

Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155					160					165

Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
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170	175	180
Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu	
185	190	195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala	
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val	
215	220	225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro	
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
275	280	285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly	
290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro	
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	
350	355	360
Ser Met Ile Pro Ser Gln Ser Arg Ala	Phe Gln Thr Val	
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

ccagtgcaca gcaggcaacg aagc 24

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln		35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala		50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr		65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser		80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys		95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys		110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro		125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys		140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp		155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro		170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln		185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val		200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro		215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu		230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu		245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile		260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys		275	280	285	

Glu Asp Val Asn	Lys Thr Leu Pro Asn	Leu Gln Val Val Asn	His
290		295	300
Gln Gln Gly Pro	His His Arg His Ile	Leu Lys Leu Leu Pro	Ser
305		310	315
Met Glu Ala Thr	Gly Gly Glu Lys Ser	Ser Thr Pro Ile Lys	Gly
320		325	330
Pro Lys Arg Gly	His Pro Arg Gln Asn	Leu His Lys His Phe	Asp
335		340	345
Ile Asn Glu His	Leu Pro Trp Met Ile	Val Leu Phe Leu Leu	Leu
350		355	360
Val Leu Val Val	Ile Val Val Cys Ser	Ile Arg Lys Ser Ser	Arg
365		370	375
Thr Leu Lys Lys	Gly Pro Arg Gln Asp	Pro Ser Ala Ile Val	Glu
380		385	390
Lys Ala Gly Leu	Lys Lys Ser Met Thr	Pro Thr Gln Asn Arg	Glu
395		400	405
Lys Trp Ile Tyr	Tyr Cys Asn Gly His	Gly Ile Asp Ile Leu	Lys
410		415	420
Leu Val Ala Ala	Gln Val Gly Ser Gln	Trp Lys Asp Ile Tyr	Gln
425		430	435
Phe Leu Cys Asn	Ala Ser Glu Arg Glu	Val Ala Ala Phe Ser	Asn
440		445	450
Gly Tyr Thr Ala	Asp His Glu Arg Ala	Tyr Ala Ala Leu Gln	His
455		460	465
Trp Thr Ile Arg	Gly Pro Glu Ala Ser	Leu Ala Gln Leu Ile	Ser
470		475	480
Ala Leu Arg Gln	His Arg Arg Asn Asp	Val Val Glu Lys Ile	Arg
485		490	495
Gly Leu Met Glu	Asp Thr Thr Gln Leu	Glu Thr Asp Lys Leu	Ala
500		505	510
Leu Pro Met Ser	Pro Ser Pro Leu Ser	Pro Ser Pro Ile Pro	Ser
515		520	525
Pro Asn Ala Lys	Leu Glu Asn Ser Ala	Leu Leu Thr Val Glu	Pro
530		535	540
Ser Pro Gln Asp	Lys Asn Lys Gly Phe	Phe Val Asp Glu Ser	Glu
545		550	555
Pro Leu Leu Arg	Cys Asp Ser Thr Ser	Ser Gly Ser Ser Ala	Leu
560		565	570

Ser Arg Asn Gly Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val
575 580 585

Leu Arg Gln Val Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe
590 595 600

Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile
605 610 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu
620 625 630

Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu
650 655

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtagcagtgc acatgggggtg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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 ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200
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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

50					55					60				
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly
				65					70					75
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala
				80					85					90
Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr
				95					100					105
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe
				110					115					120
Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly
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His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr
				140					145					150
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe
				155					160					165
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys
				170					175					180
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala
				185					190					195
Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg
				200					205					210
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu
				215					220					225
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His
				230					235					240
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala
				245					250					255
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile
				260					265					270
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His
				275					280					285
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg
				290					295					300
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr
				305					310					315
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu
				320					325					330
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala

	335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala			
	350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr			
	365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr			
	380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val			
	395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe			
	410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg			
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Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp			
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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

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<400> 72

cgttcaatgc agaaatgatc cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

cccacgcgtc cgtcctagtc cccgggccaa ctcgacagtc ttgctcattt 50

attgcaacgg tcaaggctgg cttgtgccag aacggcgcgc gcgcgcgcac 100

gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150

gctcagcggc ggcgcgggcg ctgcgcgagg gctccggagc tgactcgccg 200

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gtgggatggt gcagcgctcg ccgcggggcc cgagagctgc tgactgaag 300

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gaaat 3305

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<212> PRT
<213> Homo sapiens

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Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala
35 40 45
Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
50 55 60
Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
65 70 75
Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
80 85 90
Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
95 100 105
Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
110 115 120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
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Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly
410 415 420

Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys
425 430 435

Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala
440 445 450

Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu
455 460 465

Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg
470 475 480

Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala
485 490 495

Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser
500 505 510

Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr
515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro
530 535 540

Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro
545 550 555

Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys
560 565 570

Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly
575 580 585

Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr
590 595 600

Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr
605 610 615

His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu
620 625 630

Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln
635 640 645

Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln
650 655 660

Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys
665 670 675

Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly
680 685 690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

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<211> 483

<212> DNA

<213> Homo sapiens

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<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

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gagaccctgc caccattcc atntccatcc aag 483

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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catgagcatg tgcacggc 18

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tacctgcacg atgggcac 18

<210> 79
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<400> 79
cactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
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<400> 81
tccctggttg actctgcagc ttcc 24

<210> 82
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<212> DNA
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cttcgctggg aagagtttg 19

<210> 83
<211> 50
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gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

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atgatctgcc cgctcggcc tcccaaagtg ctgggattac aggcgagtgc 150
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 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
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 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
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 Ala Leu Leu His Leu Tyr His
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 cacaacttca gctttgcac acgagtcttg tattccaaga aaatcaaagt 2900
 ggtacaattt gtttgtttac actatgatac tttctaaata aactcttttt 2950
 ttttaa 2956

<210> 90
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90
 Met Pro Ala Arg Pro Gly Arg Leu Leu Pro Leu Leu Ala Arg Pro
 1 5 10 15
 Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Gly His Gly Gly
 20 25 30
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
 35 40 45

Ala	Asp	Gly	Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro	
				50					55					60	
His	Ser	Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	
				65					70					75	
Gln	Ser	Ala	Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	
				80					85					90	
His	Cys	Gln	Arg	Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	
				95					100					105	
Tyr	Asn	Ser	Met	Glu	Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	
				110					115					120	
Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly	
				125					130					135	
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys	
				140					145					150	
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu	
				155					160					165	
Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu	
				170					175					180	
Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	
				185					190					195	
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	
				200					205					210	

Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	
				215					220					225	
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	
				230					235					240	
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	
				245					250					255	
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	
				260					265					270	
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	
				275					280					285	
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	
				290					295					300	
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	
				305					310					315	
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	
				320					325					330	

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
425 430

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 91
atgttccttcg cgccctgggtg 20

<210> 92
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
ccaagccaac acactctaca g 21

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
aagtggtcgc cttgtgcaac gtgc 24

<210> 94
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtcaaaggg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

<400> 96
cttttctgag gaaccacagc aatgaatggc ttgcatcct tgcttcgaag 50
aaaccaatatt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150
atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200

agagggaaag catggcaaag tgggacgcat ggggccgaaa ggaattaaag 250
gagaactggg tgatatggga gatcagggca atattggcaa gactggggccc 300
attgggaaga agggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350
agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaaat 400
ttgttggaaca actggatatt agtattgctc ggctcaagac atctatgaag 450
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ctacatcgtg caggaagaga agaactacag ggaatcccta acccactgca 550
ggattcgggg tggaatgcta gccatgccca aggatgaagc tgccaacaca 600
ctcatcgctg actatgttgc caagagtggc ttctttcggg tgttcattgg 650
cgtgaatgac cttgaaaggg agggacagta catgtccaca gacaacactc 700
cactgcagaa ctatagcaac tggaatgagg ggaacccag cgaccctat 750
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agagtgccat cttaccatgt actttgtctg tgagttcatc aagaagaaaa 850
 agtaacttcc ctcatcctac gtatttgcta ttttcctgtg accgtcatta 900
 cagttattgt tatccatcct ttttttcctg attgtactac atttgatctg 950
 agtcaacata gctagaaaaat gctaaactga ggtatggagc ctccatcatc 1000
 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
 Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
 1 5 10 15
 Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200		205		210
Val Asn Asp Leu	Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn				
	215		220		225
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser				
	230		235		240
Asp Pro Tyr Gly	His Glu Asp Cys Val Glu Met Leu Ser Ser Gly				
	245		250		255
Arg Trp Asn Asp	Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys				
	260		265		270
Glu Phe Ile Lys	Lys Lys Lys				
	275				

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
 cgctgactat gttgccaaga gtgg 24

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 99
 gatgatggag gctccatacc tcag 24

<210> 100
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 100
 gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 101
 gggttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtgggtg 100
gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150
gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250
gctccatggc tgcctcctg ctgctgcccc tgctgctgtt gctaccgctg 300
ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350
cttggccttt gcggtgcgag ctctgtgctg caaaagggtt cttcgagctc 400
gcgcctggc cgcggctgcc gccgaccgg aaggtccga ggggggctgc 450
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ccgcctgcg ccggggcccc ctgctgcact gcctccgag ctgcggcgcg 900
cgcgcgctgg tgctggcgcc agagtctctg gagtccctgg agccggacct 950
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tggtgctgaa atccaagttc tcggctggtc agttctggga agattgccag 1350
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tgtcaaccag cccccgagca aggcagaacg tggccataag gtccggctgg 1450

cagtgggcag cgggctgcgc ccagatacct gggagcgttt tgtgcggcgc 1500
ttcgggcccc tgcaggtgct ggagacatat ggactgacag agggcaacgt 1550
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catggcccaa cttgtttatt gcag 2574

<210> 102
<211> 730
<212> PRT
<213> Homo sapiens

<400> 102
Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser
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Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
20 25 30

Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
35 40 45

Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
50 55 60

Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
65 70 75

Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
80 85 90

Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro
95 100 105

Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
110 115 120

Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
125 130 135

Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
140 145 150

Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
155 160 165

Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
170 175 180

Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
185 190 195

Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
200 205 210

Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly Pro
215 220 225

Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg
230 235 240

Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His
245 250 255

Cys Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu
260 265 270

Phe Leu Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met
275 280 285

Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly
290 295 300

Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro
305 310 315

Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys
320 325 330

Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala
335 340 345

Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln
350 355 360

Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro
365 370 375

Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met
380 385 390

Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly
395 400 405

Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln
410 415 420

Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser
425 430 435

Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly
440 445 450

Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro
455 460 465

Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser
485 490 495

Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp
500 505 510

Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met
515 520 525

Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser
530 535 540

Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala
545 550 555

Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe
560 565 570

Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu
575 580 585

Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu
590 595 600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

<210> 103
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 103
 gagagccatg gggctccacc tg 22

<210> 104
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 104
 ggagaatgtg gccacaac 18

<210> 105
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
acgcgcgcat acacactcgc tctcgtttgt ccatctccct cccgggggag 150
ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgc 200
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gctgcgagaga ggtccgccag gcgtacggtg ccaagggatt cagcctggcg 700
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gcagattatg gctctccgtg tgatgaccaa caaactaaaa aacgcctaca 2000
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gggagtggca gtgggtgcat ggatgacgtg tgtcccacgg agtttgagtt 2100
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 cttctgcagc ccagcgtggc cactccctgc tctcctggtc tctcacctgc 2200
 attgtcctgg cactgcagag actgtgcaga taatcttggg tttttgtca 2250
 gatgaaactg catttttagct atctgaatgg ccaactcact tcttttctta 2300
 cactcttga caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350
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 gggtgccaga ctgaactgct tcctctttcc ttcagctatc tgtggggacc 2450
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550
 gtgagggttt ttttttctc atttaaaat 2579

<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu
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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys
				20					25					30

Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala
				35					40					45

Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys
				50					55					60

Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu
				65					70					75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr
				80					85					90

Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe
				95					100					105

Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu
				110					115					120

Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn
				125					130					135

Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr
				140					145					150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp
155 160 165

Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr
170 175 180

His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp
185 190 195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln
200 205 210

Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu
215 220 225

Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro
230 235 240

Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro
245 250 255

Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys
260 265 270

Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp
275 280 285

Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu
290 295 300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile
305 310 315

Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser
320 325 330

Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys
335 340 345

Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe
350 355 360

Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr
365 370 375

Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu
380 385 390

Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr
395 400 405

Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu
410 415 420

Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile
425 430 435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp	
				440					445					450	
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met	
				455					460					465	
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly	
				470					475					480	
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser	
				485					490					495	
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe	
				500					505					510	
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg	
				515					520					525	
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser	
				530					535					540	
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg	
				545					550					555	

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

aagcgtgaca gcgggcacgt c 21

<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgacacgtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

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<210> 114
 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 114

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Gln	Ala	Cys	Val	Cys	Pro	Gly	Lys	Met	Leu	Ala	Met	Gly	Ala	Leu
				20					25					30

Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser
				35					40					45

Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala
				50					55					60

Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln
				65					70					75

Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp
				80					85					90

Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys
				95					100					105

Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro
				110					115					120

Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln
				125					130					135

Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro
				140					145					150

Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys
155 160 165

Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly
170 175 180

Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr
185 190 195

Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr
200 205 210

Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn
215 220 225

Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln
230 235 240

Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro
245 250 255

Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser
260 265 270

Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile
275 280 285

Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu
290 295 300

Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly
305 310 315

Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly
320 325 330

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys
335 340 345

Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His
350 355 360

Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val
365 370 375

His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly
380 385 390

Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu
395 400 405

Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His
410 415 420

Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln
425 430 435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu
440 445 450

Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr
455 460 465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly
470 475 480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe
485 490 495

Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr
500 505 510

Gly Ile Gln Glu Ser
515

<210> 115

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

cccaacccaa ctgtttacct ctgg 24

<210> 116

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

gccaccctac ctcagaaact gaaggagggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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gcggccagtg caaggcatca cgggttggtta gcatcggcac gtcagcctgg 250

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acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggg 350

gagtgcgtgg gaccaaacia atgcagatgc tttccaggat acaccgggaa 400

aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450

aacacagatg tgtgaataca cacggaagct acaagtgctt ttgcctcagt 500

ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550

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aagatgtgtg aacacatttg gaagctacta ctgcaaattg cacattgggt 750

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cctggtacca tcaaagacag aatcaagaag ttgcttgctc acaaaaacag 1000

catgaaaaag aaggcaaaaa ttaaaaatgt taccacagaa cccaccagga 1050

ctcctacccc taaggatgaac ttgcagccct tcaactatga agagatagtt 1100

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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly		20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
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Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
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<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gggagctgct gctgtggctg ctggtgctgt ggcgctgct cctgctcttg 50

gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300
aagatatact tgttttgccc cttgacctga ccgacctgg ttcccatgaa 350
gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400
caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450
atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500
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actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150
gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
				20					25					30

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40					45

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55					60

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val			
				65						70				75			
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly			
				80						85				90			
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr			
				95						100				105			
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr			
				110						115				120			
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile			
				125						130				135			
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser			
				140						145				150			
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn			
				155						160				165			
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser			
				170						175				180			
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser			
				185						190				195			
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln			
				200						205				210			
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile			
				215						220				225			

Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro			
				230						235				240			
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala			
				245						250				255			
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe			
				260						265				270			
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys			
				275						280				285			

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgt actatgggcc gaggggcagg gacgacgccc agaatg 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50
ggcaggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100
caatcaatcc aacagcatat tcggttgcac cttctacaca ctacagctat 150
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
tccctggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250
cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300
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gctaagaggc actgagccct caacccaagc caggctgacc tcctctgctt 400
tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450
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aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctggtg 550
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aacagaactg aattcctggt cagtggctct gggttctctg cagcgtgagg 650
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 cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300
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 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
1				5					10					15

Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser	Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu	Pro Gln Gly Lys Ala	Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu	Trp Pro Trp Gln Ala	Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys	Ser Gly Ser Leu Val	Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His	Cys Phe Glu Lys Ala	Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val	Val Leu Gly Ser Leu	Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu	Glu Val Gly Val Ala	Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His	Tyr Ser Gln Gly Ser	Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro	Thr Thr His Thr Pro	Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe	Pro Phe Gly Ala Ser	Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr	Ser Asp Ala Pro Gly	Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile	Ser Arg Pro Thr Cys	Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg	His Leu Ser Asn Pro	Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro	Gln Pro Gly Val Gln	Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro	Val Leu Cys Leu Glu	Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile	Ile Ser Phe Ala Ser	Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu	Leu Thr Asn Thr Ala	Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val	Gln Gly Ala Ala Phe	Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met	Ser Asp Glu Asp Ser	Cys Val Ala Cys Gly	305	310	315

Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp
320 325 330

Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly
335 340 345

Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys
350 355 360

Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly
365 370 375

Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly
380 385 390

Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu
395 400 405

Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys
410 415 420

Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp
425 430 435

Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln
440 445 450

Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu
455 460 465

His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
470 475 480

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu
485 490 495

Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu
500 505 510

Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg
515 520 525

Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser
530 535 540

Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu
545 550 555

Ala Glu Pro Gly Ser Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser
560 565 570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctogagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gtttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcacc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggccccc ttcgggcggg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtcac agagtcggcg cggcgcggca 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgcgt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200

ccctgggagc actgtggttc tgccctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgggtggc actggtgggc accgatgcc aacctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agataccaaa cagctgggtgc acagctttgc tgagggccag 400

gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcattcc tgaggctgca gcgcgtgcgt gtggcgagac 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

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acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950

attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met	Leu	Arg	Arg	Arg	Gly	Ser	Pro	Gly	Met	Gly	Val	His	Val	Gly
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Ala	Ala	Leu	Gly	Ala	Leu	Trp	Phe	Cys	Leu	Thr	Gly	Ala	Leu	Glu
			20						25					30

Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp
			35						40					45

Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu
			50						55					60

Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
			65						70					75

Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala
			80						85					90

Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
			95						100					105

Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe
			110						115					120

Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser
			125						130					135

Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu
			140						145					150

Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys
			155						160					165

Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp
			170						175					180

Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met
			185						190					195

Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val
			200						205					210

Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro
			215						220					225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	230	235	240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	245	250	255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	260	265	270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	275	280	285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	290	295	300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile	305	310	315

Ala

<210> 138
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
 ctggcacagc tcaacctcat ctgg 24

<210> 139
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 139
 gctgtctgtc tgtctcattg 20

<210> 140
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 140
 ggacacagta tactgaccac 20

<210> 141
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
tgcaaccag gcagctgtaa gtgc 24

<210> 142
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttagagg 150
acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250
agtgaattt gaagttctcc agaagccatt catctgcat cgcaagacca 300
aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350
ggctccttat ttcactccac tcacaaacat aacaatggc agccatttg 400

gtttaccctg ggcacccctg aggcctctcaa aggttgggac cagggcttga 450
aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tcctgctctg 500
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cattccaaga aatggatcct aatgatgact ggaaactctc taaagatgag 650
gttaaagcat atttaaagaa ggagtttgaa aaacatgggt cggtggtgaa 700
tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750
aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800
gagttataga gatacatcta cccctttta atagcactca tctttcaaga 850
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tgctttgttt tttattttta tatatTTTT ctgactccta tttaaagaac 950
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aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttactttc 1050
acagatatga agctttgttt tactttctca cttataaatt taaaatgttg 1100
caactgggaa tataaccagc catgagacca gggttatagca caaattagca 1150
ccctatattt ctgcttcctt ctatttctc caagttagag gtcaacattt 1200

gaaaagcctt ttgcaatagc ccaaggcttg ctattttcat gttataatga 1250
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<210> 145
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 145

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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20					25						30

Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
				35					40					45
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
				50					55					60
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
				65					70					75
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
				80					85					90
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
				95					100					105
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
				110					115					120
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
				125					130					135
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
				140					145					150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
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Leu

<210> 146
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 146
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<210> 147
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 147
 gccagagca ggaggaatga tgagc 25

<210> 148
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 148
 gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
 <211> 2196
 <212> DNA
 <213> Homo sapiens

<400> 149
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tttttttagc atccaacccat tcttcccttg tagttctcgc cccctcaa 100
caccctctcc cgtagccccc cgcactaaca tctcagtcctc tgaaaatgca 150
cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200
tctttttctc tttggtgcca ccaggacgga gcatggaggt cacagtacct 250
gccacccctca acgtcctcaa tggctctgac gcccgcctgc cctgcacctt 300
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350
accaggagtg caacaactgc tctgaggaga tgttcctcca gttccgcatg 400
aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450
agggaaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500
cggaggatga ggggatttac aactgctaca tcatgaaccc ccctgaccgc 550
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tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr
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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
			20						25					30

Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45

Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60

Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75

Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90

Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105

Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
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	110		115		120									
Asp	Glu	Gly	Ile	Tyr	Asn	Cys	Tyr	Ile	Met	Asn	Pro	Pro	Asp	Arg
				125					130					135
His	Arg	Gly	His	Gly	Lys	Ile	His	Leu	Gln	Val	Leu	Met	Glu	Glu
				140					145					150
Pro	Pro	Glu	Arg	Asp	Ser	Thr	Val	Ala	Val	Ile	Val	Gly	Ala	Ser
				155					160					165
Val	Gly	Gly	Phe	Leu	Ala	Val	Val	Ile	Leu	Val	Leu	Met	Val	Val
				170					175					180
Lys	Cys	Val	Arg	Arg	Lys	Lys	Glu	Gln	Lys	Leu	Ser	Thr	Asp	Asp
				185					190					195
Leu	Lys	Thr	Glu	Glu	Glu	Gly	Lys	Thr	Asp	Gly	Glu	Gly	Asn	Pro
				200					205					210
Asp	Asp	Gly	Ala	Lys										
				215										

<210> 151
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 ccnactaaca tctcagtcctc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcaagc gggctcagtc tctttttctc tttggtgcca 200
 ccaggacgga gcatggagggt ccacagtacc tgnccaccct caacgtcctc 250
 aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400
 tggagcggtt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
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gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100
cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcggtt 250
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300
tcggtgatgc tgagaaacgt gcagccggag gatgagggga ttacaactg 350
ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgccctgccct gcaccttcaa ctccctgtac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

tgcggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50

gggctgctcc cggatggcct cctgttcctc ttgctgctgc taatgctgct 100

cgcggaacca gcgctcccgg ccggacgtca cccccagtg gtgctggtcc 150

ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200

gtgcactacc tctgctccaa gaagaccgaa agctacttca caatctggct 250

gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300

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gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttcct 400

ggaccccagc aaaagcagcg tgggttccta ttccacacc atggtggaga 450

gccttggtgg ctggggctac acacgggggtg aggatgtccg aggggctccc 500

tatgactggc gccgagcccc aaatgaaaac gggccctact tcctggccct 550

ccgcgagatg atcgaggaga tgtaccagct gtatgggggc ccctggtgc 600

tggttgccca cagtatgggc aacatgtaca cgctctactt tctgcagcgg 650

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tgcgcctcgg gggggcgtgg ccaagaccct gcgcgtcctg gcttcaggag 750

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cggcaggaca cagaagggt ggtggaagcc acgatgccac ctggcgtgca 1000

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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
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	245		250		255
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu		
	260		265		270
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr		
	275		280		285
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln		
	290		295		300
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu		
	305		310		315
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys		
	320		325		330
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu		
	335		340		345
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp		
	350		355		360
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln		
	365		370		375
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser		
	380		385		390
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu		
	395		400		405

Lys Arg Val Leu Leu Gly Pro
410

<210> 158
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 158
ctggggctac acacggggtg agg 23

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 159
ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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atggagagcg gggcctacg cgcgccaag gcggcggt ccttcgacct 100
gcggcgcttc ctgacgcagc cgaggtggt ggcgcgcgc gtgtgcttg 150
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<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162

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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40					45

Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55					60

Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70					75

Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85					90

Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val
				95					100					105

Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115					120

Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130					135

Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145					150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
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Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

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<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

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<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

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aactccagct ccgtctattc ctttggggag ggacccctca cctgcttctt 500

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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu				

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Thr Ala Lys Ala Gln Lys Met Leu Lys	Glu Leu Ile Thr Ser Thr	
110	115	120
Arg Leu Gly Thr Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe Gly	
125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile Pro	
140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro	Glu Val Val Gln Ala Leu	
155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala Val	
170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val Ile	
185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr Leu	
200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu Arg	
215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser	Ser Cys Leu Trp His Leu	
230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp Thr	
245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala Gly	
260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser Arg	
275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala	Ser Gly Ala Ile Met Ala	
290	295	300
Val Val Trp Lys Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe Val	
305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln	Ala Cys Glu Val Asn Leu	
320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr Pro	
335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp His	
350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe Asp	
365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr Gln	

380										385					390				
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile					
				395					400					405					
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly					
				410					415					420					
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
				425					430					435					
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
				440					445					450					
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys					
				455					460					465					
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys					
				470					475					480					
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile					
				485					490					495					
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly					
				500					505					510					
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe					
				515					520					525					
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro					
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Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu					
				545					550					555					
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly					
				560					565					570					
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu					
				575					580					585					
Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp					
				590					595					600					
Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met					
				605					610					615					
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln					
				620					625					630					
Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu					
				635					640					645					
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val					
				650					655					660					
Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val					

665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly		
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly		
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro		
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg		
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln		
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg		
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg		
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser		
785	790	795
Trp Ile Gln Gln Val Val Thr		
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 <212> DNA
 <213> Homo sapiens

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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc cactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 176

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<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

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aaaaaaaaaa 1510

<210> 178
<211> 354
<212> PRT
<213> Homo sapiens

<400> 178

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Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg
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Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val
35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu
95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val
110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val
125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro
200 205 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser
215 220 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
230 235 240

Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn
245 250 255

Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val
260 265 270

Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
275 280 285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro
350

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcott ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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acgcgctgga ggagtggagc agcaccggc cgccctggg ggctgacagt 150
cggcaaagtt tggcccgaag aggaagtggc ctcaaacc cggcaggtggc 200
gaccaggcca gaccaggggc gctcgctgcc tgcgggcggg ctgtaggga 250
gggcgcgcc cagtgccgag acccggggct tcaggagccg gcccgggag 300
agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350
caccgcccct actccgggc tgcgcgcgc tccccgccc cagccctggc 400
atccagagta cgggtcgagc ccgggccatg gagccccct ggggaggcgg 450
caccaggag cctgggcgc cggggctccg ccgcgacccc atcgggtaga 500
ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550
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 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr			

	185		190		195
Leu Glu Asp Phe	Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr	His		
	200	205	210		
Leu Ala Ser Val	Ser His Pro Gln Ser	Cys His Trp Leu Leu	Asp		
	215	220	225		
Pro His Asp Gly	Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu	Asp		
	230	235	240		
Leu Gly Phe Gly	Asp Ala Val His Val	Tyr Asp Gly Pro Gly	Pro		
	245	250	255		
Pro Glu Ser Ser	Arg Leu Leu Arg Ser	Leu Thr His Phe Ser	Asn		
	260	265	270		
Gly Lys Ala Val	Thr Val Glu Thr Leu	Ser Gly Gln Ala Val	Val		
	275	280	285		
Ser Tyr His Thr	Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn	Ala		
	290	295	300		
Thr Tyr His Val	Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro	Cys		
	305	310	315		
Gly Leu Gly Ser	Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu	Arg		
	320	325	330		
Cys Tyr Ser Glu	Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys	Ala		
	335	340	345		
Asp Gly Thr Asp	Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly	His		
	350	355	360		
Phe Pro Cys Gly	Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys	Tyr		
	365	370	375		
Leu Pro Ala Asp	Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp	Gly		
	380	385	390		
Ala Asp Glu Arg	Arg Cys Arg His Cys	Gln Pro Gly Asn Phe	Arg		
	395	400	405		
Cys Arg Asp Glu	Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp	Gly		
	410	415	420		
Gln Pro Asp Cys	Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser	Tyr		
	425	430	435		
Val Leu Pro Arg	Lys Val Ile Thr Ala	Ala Val Ile Gly Ser	Leu		
	440	445	450		
Val Cys Gly Leu	Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys	Lys		
	455	460	465		
Leu Tyr Ala Ile	Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro	Leu		

470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser	
485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp	
500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu	
515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly	
530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg	
545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn	
560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser	
575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg	
590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro	
605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala	
620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro	
635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly	
650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro	
665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp	
680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu	
695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr	
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcttgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gcccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggactgata ccagaaacca caacattgac 450
 agttggtgga ggggtgtttg cacttgtagc agcagtatgc tgtcttgccg 500
 acggggccct tattaccgg aagcttctgt tcaatcccag cggtccttac 550
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600
 tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
1				5					10					15

Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
				20					25					30

Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45

Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60

Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75

Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90

Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105

Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120

Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgcccct tctgttcag tgtgaaaggc cacgtgaaga tgctgcggt 200
ggcactaact gngacatcta tgacctttt tatnatcgca caagcccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggt aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50

ggaccggcta ggctgggagc gcccccgagg ccccgccgtg ggcatgggag 100

caactggcccg ggcgctgctg ctgcctctgc tggcccagtg gctcctgagc 150

gcccggcccg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200

cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggaccctg 250

ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgcctgggag 300

tcccccgagg ggcgcgcca cttcttgagg atggtagaca acctgcaggg 350

ggactctggc cgcggtact acctggagat gctgatcggg accccccgcg 400

agaagctaca gattctcggt gacactggaa gcagtaactt tgccgtggca 450

ggaacccgcg actcctacat agacacgtac tttgacacag agagggtctag 500

cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550

gctggacggg cttcggtggg gaagacctcg tcaccatccc caaaggcttc 600

aatacttctt ttcttgtaaa cattgccact atttttgaat cagagaattt 650

ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700

cacttgccaa gccatcaagt tctctggaga ccttcttcga ctccctgggtg 750

acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagccgg 800

cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850

gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900

gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
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gtggaagctg tggcccgcgc atctctgatt ccagaattct ctgatgggtt 1100
ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttggg 1150
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atgcgctggg gatcggtgcc acgggtgatg agggcttcta cgtcatcttc 1350
gacagagccc agaagagggt gggcttcgca gcgagcccct gtgcagaaat 1400
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acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750
caccgtctt caatctctgt tctgtccca gatgccttct agattcactg 1800
tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
1				5					10					15

Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20						25					30

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala		65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg		80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu		95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly		110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser		125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr		140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile		155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile		170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly		185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser		200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro		215	220	225
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Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala		230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu		245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu		260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly		275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala		290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val		305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro		320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp		335	340	345

Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	350	355	360
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	365	370	375
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	380	385	390
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	395	400	405
Val	Ile	Gly	Ala	Thr	Val	Met	Glu	Gly	Phe	Tyr	Val	Ile	Phe	Asp	410	415	420
Arg	Ala	Gln	Lys	Arg	Val	Gly	Phe	Ala	Ala	Ser	Pro	Cys	Ala	Glu	425	430	435
Ile	Ala	Gly	Ala	Ala	Val	Ser	Glu	Ile	Ser	Gly	Pro	Phe	Ser	Thr	440	445	450
Glu	Asp	Val	Ala	Ser	Asn	Cys	Val	Pro	Ala	Gln	Ser	Leu	Ser	Glu	455	460	465
Pro	Ile	Leu	Trp	Ile	Val	Ser	Tyr	Ala	Leu	Met	Ser	Val	Cys	Gly	470	475	480
Ala	Ile	Leu	Leu	Val	Leu	Ile	Val	Leu	Leu	Leu	Pro	Phe	Arg		485	490	495
Cys	Gln	Arg	Arg	Pro	Arg	Asp	Pro	Glu	Val	Val	Asn	Asp	Glu	Ser	500	505	510

Ser Leu Val Arg His Arg Trp Lys
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<211> 21

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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ggaaattgga ggccaaagc 19

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<212> DNA
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<212> DNA
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<220>
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<400> 200
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204

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<213> Homo sapiens

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ttccggggcg atgcagggtt ggggtcatct gtatctgaag cccctcgga 1900

taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
			20						25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
			35						40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
			50						55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
			65						70					75

Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile	80	85	90
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe	95	100	105
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile	110	115	120
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe	125	130	135
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr	140	145	150
His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
365 370 375

Leu Ser

<210> 207
<211> 24
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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cttcatggcc ttggacttgg ccag 24

<210> 208
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<220>
<223> Synthetic oligonucleotide probe

<400> 208
acgccagtgg cctcaagctg gttg 24

<210> 209
<211> 45
<212> DNA
<213> Artificial Sequence

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<400> 209
ctttctgagc tctgagccac ggttgacat cctcatccac aatgc 45

<210> 210
<211> 3716
<212> DNA
<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 211

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				20					25					30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60
Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
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Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr
425 430 435

Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala
440 445 450

Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val
455 460 465

Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly
470 475 480

Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met
485 490 495

Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr
500 505 510

Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg
515 520 525

Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu
530 535 540

Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp
545 550 555

Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser
560 565 570

Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu
575 580 585

Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp
590 595 600

Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu
605 610 615

Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln
620 625 630

His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu
635 640 645

Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser
650 655 660

Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala
665 670 675

Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg
680 685 690

His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr
695 700 705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser
710 715 720

Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys
725 730 735

Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro
740 745 750

Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu
755 760 765

Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu
770 775 780

Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro
785 790 795

Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser
800 805 810

Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly
815 820 825

Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro
830 835 840

Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp
845 850 855

Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu
860 865 870

Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala
875 880 885

Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu
890 895 900

Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro
905 910 915

Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro
920 925 930

Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser
935 940 945

His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp
950 955 960

Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro
965 970 975

Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser
980 985

<210> 212
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 212
gaagggacct acatgtgtgt ggcc 24

<210> 213
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 214
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50
ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100
gcgggttcga aggggacact gtgtccctgc agtgcaccta caggaagag 150
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200
tcgctgctct ggaccatct atgcagaaga agaaggccag gagacaatga 250
agggcaggggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350
cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400
caggaccctg ctgtcctccc tccccctctc ccaccttcca gcctctggct 450
acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agcccccagg 500
attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550
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tcctgcaggg agtccccgcc ccccatgca gctggactcc acctcagcag 700
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atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800
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 cttttagtag agatgggggtt tcaccatgtt ggccaggctg gtcttgaact 2350
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 caggcatgag ccactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450
 agagttgttc agtatgcaa acttggaag atggaggaga aaaagaaaag 2500
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550

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 tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216
 <211> 332
 <212> PRT
 <213> Homo sapiens

<400> 216
 Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
 1 5 10 15
 Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
 20 25 30
 Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
 35 40 45
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg

	50		55		60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met	65		70		75
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu	80		85		90
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr	95		100		105
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile	110		115		120
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser	125		130		135
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala	140		145		150
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu	155		160		165
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu	170		175		180
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr	185		190		195
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro	200		205		210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala	215		220		225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg	230		235		240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu	245		250		255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His	260		265		270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln	275		280		285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys	290		295		300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro	305		310		315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val	320		325		330
Ser Ala					

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
ctgtcttccc ctgcttggt gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
ggtgcaggaa ggggtgggatac ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
gggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100
cagtgtgaaa gaaccagtgg tctcgtctctg ttgccaggc tagagtgtac 150
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400

gctgggatca tgttggtggc cctgggtctgt ctgctcagct gcctgctacc 450
ctccagttag gccaaactct acggtcgttg tgaactggcc agagtgtac 500
atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
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actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tgttggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggccggg cgcccgcggc ggcacatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tcctcgtctt cgcgctcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaagctgt cgtcggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc cgcggtgccc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctcttc ggcaagggtg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400
ttgcagtgc gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagccacag ggcttcaggt ggtcaggatg 500
ctctgacaac atcgctacg gtgtggcctt ctcacagtcg tttgtggatg 550
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atgcaagtgc cacgggggtgt caggctcctg tgaggtaaag acgtgctggc 700
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ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650
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cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800
agaccacct aggcaggcat ataggctgcc atcctggacc agggatcccc 1850

gctgtgcctt tgcagtcacg cccgagtcac ctttcacagc gctgttcctc 1900
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000
ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226

Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe
1 5 10 15

Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys
20 25 30

Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys
35 40 45

Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn
50 55 60

Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile
65 70 75

Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser
80 85 90

Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly
95 100 105

Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val
110 115 120

Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys
125 130 135

Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe
140 145 150

Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe
155 160 165

Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser
170 175 180

Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg
185 190 195

Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly
200 205 210

Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro

	215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly	230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu	245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu	260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg	275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser	290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe	305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe	320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val	335	340	345
Glu Leu His Thr Cys Arg	350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaaat tatcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50

gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100

gctccgagga ggtccccgga gggccctggg gacgctgggt gacttggagc 150

aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcttttg 200

ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250

cgtgcttga cgccacgac ctgctgagga caaacgcctc gaagcagacg 300

gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350

ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400

cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450

cgcgtgaccc agggcttggc tgaagccggc agggggcgtg aggacgtccg 500

cactgagctg ttccggggcg tggaggccgt gaggtccag aacaactcct 550

gcgagccgtg cccacgctg tggctgtcct tcgagggtc ctgctacttt 600

ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650

tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700

tcactcgga cagcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gactctctct 800

cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850

agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900

gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950

ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg taccctgggg 1000

gctgtcacc tccctggctc ctggagctga ttgccaaaga gttttttct 1050

tcctcatcca ccgctgctga gtctcagaaa cacttgccc aacatagccc 1100

tgtccagccc agtgccctgg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu	1	5	10	15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg	20	25	30	
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	
Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210	

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp
275 280 285

Ile Cys Glu Lys Arg His Asn Cys
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggggtgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100

ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gaccgcaccg ctgccggccg 250

cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgcgcccg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450

gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgcct cccagcggc accgggcaga cgtcggcgga gctggagggtg 700

cagcgcaggc actcgctggg ctcgtttggt gtgcgcacgtg tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca cttctcctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950

actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggctgcgac agagccccag ggccttcac cctcccggcc cagtctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccgc 1100

tggactgcga ggtctccctg tggtcgtcct ggggactgtg cggaggccac 1150

tgtgggaggc tcgggaccaa gagcaggact cgctacgtcc gggtcagacc 1200

cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250

tccctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggcccc 1300

cggagccatg ggggtgcggg ggctcctgtg caggctcatg ctgcaggcgg 1350

ccgagggcac aggggggttc gcgctgctcc tgaccgcggt gaggccgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
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 gtctgtcttc agcctcctcc tctgcagga taaagtcac cccaaggctc 1550
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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 236

Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys
 1 5 10 15

Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly
 20 25 30

Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile
 35 40 45

Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr
 50 55 60

Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
 65 70 75

Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val
 80 85 90

Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala
 95 100 105

Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val
 110 115 120

His Glu Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln
 125 130 135

Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser
 140 145 150

Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val
 155 160 165

Asp Ser Leu Asp	Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala	170	175	180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	185	190	195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	200	205	210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	215	220	225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	230	235	240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	245	250	255
Pro Val Leu Pro	Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	260	265	270
Val Pro Glu Thr	Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	275	280	285
Trp Gly Leu Cys	Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser	290	295	300
Arg Thr Arg Tyr	Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	305	310	315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	320	325	330

Val

<210> 237
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 cagcactgcc aggggaagag gg 22

<210> 238
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 238
 caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagcccccttc tcctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtcctgcggg atg 23

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagcccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894
<212> DNA
<213> Homo sapiens

<400> 244

ggcggcggtcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50
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aggaagagtg tactcgtagg cggacagctt tagtgcccg cggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc cttaaagcttg 300
cagaaatddd atccaacttt gtttgaagc ttattatgac aataccattd 350
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaattg 500
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaaggtda caggggatac 600
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650
gaccacataa tccacacaaa ataaaaagct gtgaggtttt gtttaatcct 700

tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aattttagtt 800
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850
gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900
ggatgatcca catctcagtt ctgttccagt ttagaaaagt gaaaaaggtd 950
atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050
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aagtggagaa gaaatcagtc agccgcagtd aagagctcag aaaagaagca 1150
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aggaagcaac agtcaaagaa gggaacttcc cggaagatc agacccttgc 1350
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 ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
 tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500
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 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggtg 1800
 catgtgtttt ttctagctg accttttata ttgctaaatc tgaaataaaa 1850
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val	1	5	10	15
Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser	20	25	30	
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu	35	40	45	
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly	50	55	60	
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly	65	70	75	
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg	80	85	90	
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly	95	100	105	
Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	110	115	120	
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	125	130	135	

Asp Thr Val Tyr	Asn Met Leu Arg Leu	Ser Glu Val Asp Ile	Asp
	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His	Lys Ile Lys Ser Cys	Glu
	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile	Ile Pro Arg Glu Ile	Lys
	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu	Glu Val Lys Lys Leu	Lys
	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu	Leu Ser Phe Gly Glu	Glu
	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn	Arg Val Ser Gln Ser	Met
	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp	Leu Leu Lys Asp Asp	Pro
	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu	Ser Glu Lys Gly Asp	Ala
	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp	Glu Ser Ala Glu His	Asp
	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn	Leu Met Arg Glu Arg	Ile
	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser	Ala Asn Val Lys Ser	Ala
	290	295	300
Gly Glu Gly Glu	Val Glu Lys Lys Ser	Val Ser Arg Ser Glu	Glu
	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys	Arg Glu Leu Leu Ala	Ala
	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala	Lys Gln Ala Glu Lys	Arg
	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp	Gly Ala Val Ala Glu	Tyr
	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala	Leu Arg Lys Gln Gln	Ser
	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln	Thr Leu Ala Leu Leu	Asn
	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala	Ile Ala Glu Thr Pro	Glu
	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp	Met
	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
cgccgccgtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50
gatgctgccc ggccgcctc ggctttgagg cgagagaagt gtcccagacc 100
catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200
gaccagcaca ggcggcgttt tctccttcgg aacgggaacg tctagcaacc 250
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aaaaaa 2456

<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

Met	Ser	Thr	Gly	Phe	Ser	Phe	Gly	Ser	Gly	Thr	Leu	Gly	Ser	Thr
1				5					10					15

Thr	Val	Ala	Ala	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Val	Phe	Ser	Phe
				20					25					30

Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly
				35					40					45

Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser
				50					55					60

Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly
				65					70					75

Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg
				80					85					90

Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met
				95					100					105

His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe
				110					115					120

Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro
				125					130					135

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro	140	145	150
Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg	155	160	165
Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu	170	175	180
Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu	185	190	195
Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg	200	205	210
Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val	215	220	225
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met	230	235	240
Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser	245	250	255
Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val	260	265	270
Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp	275	280	285
Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala	290	295	300
Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp	305	310	315
Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser	320	325	330
Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His	335	340	345
Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile	350	355	360
Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala	365	370	375
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg	380	385	390
Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg	395	400	405
Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

aggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100

ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150

tgcattctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250

aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300

accgggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350

cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400

gggtggagag aggaagctat gtgacatata atttcatgaa cgatggggtc 450

tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500

caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550

agaggaccgt ccgactccgt gtggcctatg cccccagaga ccttgttatc 600

agcattttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650

tgtcccatac ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700

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gcccggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850

acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900

ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtccctgga 950

aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000

gcctgggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050

cagaggggac aggttctgag cccctcccag ccctcagacc ccggggctcct 1100

ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150

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<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln
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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30

Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45

Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60

Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75

Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90

Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105

Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120

Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135

Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150

His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165

Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180

Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195

Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210

Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser
230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val
245 250 255

Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg
260 265 270

Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro
275 280 285

Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val
290 295 300

Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly
305 310 315

Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala
320 325 330

Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln
335 340 345

Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu
350 355 360

His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
365 370 375

Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu
380 385 390

Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile
395 400 405

Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile
410 415 420

Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe
425 430 435

Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr
440 445 450

Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn
455 460 465

Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser
470 475 480

Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu
485 490 495

Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu
500 505 510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

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<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
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cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
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atttaaa 2857

<210> 264
<211> 772
<212> PRT
<213> Homo sapiens

<400> 264

Met	Asn	Cys	Tyr	Leu	Leu	Leu	Arg	Phe	Met	Leu	Gly	Ile	Pro	Leu	1	5	10	15
Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys	20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	275	280	285	

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser
290 295 300

Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile
305 310 315

Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr
320 325 330

Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu
335 340 345

Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln
350 355 360

Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr
365 370 375

Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly
380 385 390

Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg
395 400 405

Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly
410 415 420

Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp
425 430 435

Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln
440 445 450

Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp
455 460 465

His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu
470 475 480

Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp
485 490 495

Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser
500 505 510

Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln
515 520 525

Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu
530 535 540

Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn
545 550 555

Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val
560 565 570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln
575 580 585

Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala
590 595 600

Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr
605 610 615

Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys
620 625 630

Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly
635 640 645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly
755 760 765

Ser Ala Val Gln Ser Asn Asn
770

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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ccgccttaa cttcctccgc ggggccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ccttctgcac ctgccacccc tgagccagcg 200
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250
cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgcctgc 300
cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350
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 gtggtcagc gccttcctct ctctaccagt ctatttccat tctttcagct 2350
 gtgtctgaca tgtttgtgct ctgttccatt ttaacaactg ctcttacttt 2400

tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450
 aggggtgttg cactggtgtc tggagacctg gatttgagtc ttggtgctat 2500
 caatcacctg ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550
 cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600
 gatgttgtgg ggatccagtg agatagaata catgtaagtg tggttttgta 2650
 atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700
 gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgттаag 2747

<210> 270
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 270
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 1 5 10 15
 Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
				200					205					210					

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
tttttagttgc cacagcatgg tatggcaata gaancnttca acantttctat 450
gaccctatga cccagtc aa tgccaggtac gaatttggtc aggctctctt 500
cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
gctgttctctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50

tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100

cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150

acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200

tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250

atctgagcag cacattgcaa gcaacccgtg ccttgatggt ggttggcatc 300

ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350

tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400

gggggcgca tatttcttct tgcaggctctg gctatttttag ttgccacagc 450

atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394

<223> unknown base

<400> 273

gggcccgacc attatccaac cgggntcaact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac ccentgccctg atgggtggtg 250
gcatcctcct gggagtata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattggggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450
cccagtcaat gccaggtacg aatttggtca ggctctcttc actggctggg 500
ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttcctgc 550
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctccct cctggatgga tcgcnccacc gtcacattgc cttccccan 50
tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccctgac cttgatggg ttggcatcct cctgggagtg atagcaacct 250
ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
cnngnnntct atgacctat gacccagtc aatgccaggt acgaatttgg 450

tcaggetctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50

gcagcacatt ncaagcaacc ccttgcccttg aagggtggtg ncatcccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300

tgccaggtac gaatttggtc aggctctctt cactggctgg gctgctgctt 350

ctctctgcct tctgggaggt gccctaactt gctgttcttg tccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

agcaatgccc tgccccagtg ggaggattaa ttcctatgnt ggggacaaca 50

ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100

cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcattcttc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgcgatatctt cttnttgacg gtctggctat tttagttgcc acagcatggt 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtagc aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataggggg gcgcgatatt ttttcttgca ggtntggta ttttagttgc 50

cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtag gaatttgggc aggcctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

ttcctgggat ggatccgccc ccactntcac atgccctgcc ccttggagat 50

ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaaccntg 200

ccttgatggt gggtggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgtg tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgaga tatttcttct tgcaggtctg 350

gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgaccca gtcaatgcca ggtaogaatt tggtcaggct 450

ctcttactg gctgggctgc tgcttctctc tgcttcttg gaggtgccct 500

actttgctgt tcctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcattctgc ttcctgggat ggaatcggcg 50
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200
aatctgagca gcacattgca agcaaccntg ccttgatggg ggttggcatc 250
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350
ggggcgcgat atttcttctt gcaggctctg ctatttntag ttgccacagc 400
atgggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttactggt ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttctgttt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 282
ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283
<211> 2285
<212> DNA
<213> Homo sapiens

<400> 283
gcgtgccgtc agctcgccgg gcaccgcggc ctcgccctcg cctccgccc 50
ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100
tagaggaccc ccgcccgtgc cccgaccggt ccccgcttt ttgtaaaact 150
taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200
ctccccgcca aagggtgctc gccgctaagg aacatggcga aggtggagca 250
ggctctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300
ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950
aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattggtg 1000
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaa ttaccctcc 1100
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200
ctttattaat gacaaggaa accatgagta atgccacaat ggcatattgt 1250
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc ccttggggag 1350
ctggagccca gcatgctggg gaggcggtc agctccacac agtagtccc 1400
acgtggccca ctcccgccc aggtgctttt ccgtgtcttc agttctgtcc 1450
aagccatcag ctcttgga ctgatgaaca gagtcagaag cccaaggaa 1500
ttgcaactgtg gcagcatcag acgtactcgt cataagtga aggcgtgtgt 1550
tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttact 1600
taaagggacc aagctaaatt tgtattggt catgtagtga agtcaaactg 1650
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcact 1700
catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750
ctctgttggg tgaactgta ttgctgctgg agggctgtgg gctcctctgt 1800
ctctggagag tctggcatg tggaggtgg gtttattggg atgctggaga 1850
agagctgcca ggaagtgtt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctaggta ctttttttaa 1950
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggtagaa 2100
gagagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Leu Lys Phe Arg Gly	Pro Phe Thr Asp	Val Val Thr Thr Asn	Leu
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Lys Leu Gly Asn Pro	Thr Asp Arg Asn	Val Cys Phe Lys	Val Lys
35		40	45
Thr Thr Ala Pro Arg	Arg Tyr Cys Val	Arg Pro Asn Ser	Gly Ile
50		55	60
Ile Asp Ala Gly Ala	Ser Ile Asn Val	Ser Val Met Leu	Gln Pro
65		70	75
Phe Asp Tyr Asp Pro	Asn Glu Lys Ser	Lys His Lys Phe	Met Val
80		85	90
Gln Ser Met Phe Ala	Pro Thr Asp Thr	Ser Asp Met Glu	Ala Val
95		100	105
Trp Lys Glu Ala Lys	Pro Glu Asp Leu	Met Asp Ser Lys	Leu Arg
110		115	120
Cys Val Phe Glu Leu	Pro Ala Glu Asn	Asp Lys Pro His	Asp Val
125		130	135
Glu Ile Asn Lys Ile	Ile Ser Thr Thr	Ala Ser Lys Thr	Glu Thr
140		145	150
Pro Ile Val Ser Lys	Ser Leu Ser Ser	Ser Leu Asp Asp	Thr Glu
155		160	165
Val Lys Lys Val Met	Glu Glu Cys Lys	Arg Leu Gln Gly	Glu Val
170		175	180
Gln Arg Leu Arg Glu	Glu Asn Lys Gln	Phe Lys Glu Glu	Asp Gly
185		190	195
Leu Arg Met Arg Lys	Thr Val Gln Ser	Asn Ser Pro Ile	Ser Ala
200		205	210
Leu Ala Pro Thr Gly	Lys Glu Glu Gly	Leu Ser Thr Arg	Leu Leu
215		220	225
Ala Leu Val Val Leu	Phe Phe Ile Val	Gly Val Ile Ile	Gly Lys
230		235	240
Ile Ala Leu			

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

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tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200
cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50
gattacctcc ttaaattgaca ccttcctcg cctgttggtg ctggccttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagcca 250
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag ctaaattgta ttggttcag tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
gggtggcccat tcccggccca ggctgctttc cggtnttcag ttctgtccaa 50
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgcctt tgttcantta 200
aagggaacaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttggggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
atttaactta tttaatgtat ttcattcat gttttcttat tgtcacaaga 300
gtacagttaa tgctgcgtgc 320

<210> 290
<211> 609
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598
<223> unknown base

<400> 290
aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
gaaaccntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
cttctctgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200
ggggagtgcg gtctgctcca cacagtatgc ccangtggc ccantcccgg 250
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ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
cagangtant ngtcataagt gagaggcgtg tggtgantga ttgaccagc 400
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
atgcatattt aantattta atgtatttca tntcatgttt tcttattgtc 550
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gtattgctg 609

<210> 291
<211> 493
<212> DNA
<213> Homo sapiens

<400> 291

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cacagtagtc cccacgtggc ccactcccgg cccaggctgc tttccgtgtc 100
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
gagaggcgtg tgttgactga ttgaccacgc gctttggaaa taaatggcag 250
tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
gcgtgctgct gaactctgtt ggggtgaactg gtattgctgc tggagggctg 450
tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggtca 50
ggctggctga gaggtccca gctgcagcgt ccccgccgc ctcccgga 100
gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
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atctttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350
atcttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400
ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450
tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500
ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550
cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600
aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgatg 650
gcaccgacag cagggtcagc atcttgga aaaggttctt aaccaatttc 700
cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750
ttcccctcag catgttctaa ctgctgcca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850
aataaaagtg gaggaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagagggtac cagagagcat ctgcaggaga 950
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tggatgtcca cgggggttcag aaggactaca acgttgctgt tcgcatcact 1450
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 accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850
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 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
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 ttcagctcat gccctcaatg tttatattgt gttatctgtt gggctctggga 2050
 catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
 caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200

cctagttagt aaatagggaa gctgagacat tttaagatct caagtittta 2250
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 cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
1				5				10					15	

Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

	20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu	35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr	50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu	65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn	80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu	95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg	110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp	125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu	140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu	155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly	170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser	185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala	200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu	215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln	230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys	245	250	255
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp	260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala	275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys	290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp			

	305		310		315
Arg Ala Asp Gln	Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp	Glu		
	320		325		330
Ser Asn Asp Leu	Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly	Ser		
	335		340		345
Thr Gly Ser Gly	Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys	Lys		
	350		355		360
Asn Trp Lys Arg	Lys Ile Ile Ala Val	Tyr Ser Gly His Gln	Trp		
	365		370		375
Val Asp Val His	Gly Val Gln Lys Asp	Tyr Asn Val Ala Val	Arg		
	380		385		390
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His	Gly		
	395		400		405
Asn Asp Ala Asn	Cys Ala Tyr Gly				
	410				

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaaggaggc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300

aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgtttagca 50
ccagtactgg atgtgacagc aggacagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
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ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
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gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500
ccaagccaaa ggaacaacc tggttggtga actagcacct aaggtcttag 550
atggtacgcg ttgtatata gaatctttgg atatgtgcat cagtggttta 600
tgccaaattg ttggctgcca tcaccagctg ggaagcaccg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700
ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtggtt 750
gcacttcctt atggaagtag acatattcgc cttgtcttaa aaggtcctga 800
tcacttatat ctggaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttggtg acaattctag tgtggacttc 900
cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
agatttcatt gtcaagattc gtaactcggg ctccgctgac agtacagtcc 1000
agttcatctt ctatcaacc atcatccacc gatggaggga gacggatttc 1050
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gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150
attaccaga gaacatcaaa cccaaacca agcttcagga gtgcaacttg 1200
gatccttgct cagccagtga cggatacaag cagatcatgc cttatgacct 1250
ctaccatccc cttcctcggg gggaggccac cccatggacc gcgtgctcct 1300

cctcgtgtgg ggggggcatc cagagccggg cagtttcctg tgtggaggag 1350
gacatccagg ggcattgtcac ttcatgtgaa gaggaggaaat gcatgtacac 1400
ccctaagatg cccatcgcgc agccctgcaa cttttttgac tgccttaaata 1450
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agataccgtg tggtcctctg catcgaccat cgaggaaatgc acacaggagg 1550
ctgtagccca aaaacaaagc cccacataaa agaggaaatgc atcgtaccca 1600
ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650
tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700
gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750
gtttaaagaa agcagtggtct cactgggtgt agctttcatg ggttctgaac 1800
taagtgaat catctacca aagctttttg gctctcaaata taaagattga 1850
ttagtttcaa aaaaaaaaaa 1869

<210> 301
<211> 525
<212> PRT
<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
1				5					10					15

Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30

Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45

Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75

Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90

Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105

Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120

Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtggggc 50
 ctggggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctggggcggg cgctgtggct ggcggccccg cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggacccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
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 gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500
 tccagtgcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
 caaaagttca gctcccagca ggattgtggg agtttcttcc aaactttata 650
 aatacggaga catcaatctt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagccg gagcaaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
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 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
 agtgatgggt ggctgtctaa aataggaaca aggagtaaaa gagctgttta 1100
 taaaactgca tatcagttat atctgtgatc aggaatgggtg tggattgaga 1150
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 ggtacatgtg ggtattttgg agttactgaa aaattatit tgggataaga 1250
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 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaatatit gtcagaatta agtgactcaa agtgctatcg 1400
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttgggtgt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
 cacaagtctt acttggaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
1				5				10				15		
Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20					25						30
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
			35					40						45
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
			50					55						60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
			65					70						75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
			80					85						90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly

	95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg	110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg	125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr	140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His	155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys	170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr	185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser	200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile	215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val	230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly	245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu	260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr	275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly	290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala	305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val	320	325	330
Met Val Gly Leu Leu Lys	335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcagggg tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccctttccta acccaacca acctagccca gtcccagccg 100
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttcctatcc ttacccgacc tcagatgctc ctttctgctc ctggttaactt 200
gggtttttac tctgttaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaacaa tgctgatgtt gctttagtaa atttttatgc 300
tgactgggtg cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650

cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttacia ttggattcaa 850
gataaatgtg ttctctttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacct gccgattgtg acaaatttag 1050
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
 gcttttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	20	25	30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	
Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195	

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 48
 <223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgngg agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccttttcta acccaacca acctagccn gtcccagccg 150
ccagcgcctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccogacc tcagatgctc ctttctgctc ctggtaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaacna tgctgatgtg gcttttagtca atttttatgc 350

tgactgggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 318
ctgtatctct gggctatgtc agag 24

<210> 319
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 319
ctacatataa tggcacatgt cagcc 25

<210> 320
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 320
cgtcttccta tccttaccgc acctcagatg ctcccttctg ctcttg 46

<210> 321
<211> 1333
<212> DNA
<213> Homo sapiens

<400> 321
gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50
cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100
gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150
taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200
gtgtcatggt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250
cccctcttgg catatcatat ttggaggat atgagtagac cagtgatgag 300
tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350
catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400
tttttttact acctatatgg catgatctat gttttgggtga gctcttagaa 450
caacacacag aagaattggc ccagttaagt gcatgcaaaa agccaccaa 500
tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550
tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttccacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaactt catgggtttc ctcactgtgc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt ctttaagcata agtaaacaatg atataaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaattgtgt 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5				10					15	

Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20				25					30	

Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35				40					45	

Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50				55					60	

Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65				70					75	

Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80				85					90	

Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95				100					105	

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtgggttaca ctgggtctca 150
atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200
atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450

gaatctgatc agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag ggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggaccaact ggggctcccg ccgctgctgc tgctgacat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttgggtgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500
 aactctgggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
 gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
 ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
 aactcttgct ctctcggtga tggatttgct ttggatttgc tgtgcaactg 850
 ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttggt gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgaat agacatctaa aattcactc ctcatagagc 1100
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
 caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10					15
Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
				20					25					30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
				35					40					45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
				50					55					60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
				65					70					75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
				80					85					90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
				95					100					105

Gln Ser Asp Glu Gln Tyr Ala Cys His	Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu	Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu	Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln	Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp	Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala	Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu	Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg	Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu	Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser	Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala	Val Glu Gln Tyr Val Pro	260	265	270

Ser Glu Lys Leu Ser Ile Tyr Gly Asp	Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser	Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala	Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile		320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccggggc tgtcagttga cctacccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatacga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
tttctcttaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

<400> 332
cacactggcc ggatctttta gagtcctttg accttgacca agggtcngga 50
aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100
cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150
tgctgaccat ggccttggcc ggagggttcgg ggaccgcttc ggctgaagca 200
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
agagaggttg caggctgttt tcaatttgtc agtttggtga tgatggaatt 350

gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
ttcccaatct gatgagcaat atgcttgcca tcttgggtgc cagaatcagc 450
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
gatggactcc gc 562

<210> 333
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 333
acaagctgag ctgctgtgac ag 22

<210> 334
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cggcccggag gtggggcgcc gctggggccg gcccgcacgg gttcatctg 100
aggggcgacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccc cggtctggga ttcttgtttg 200

gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccgaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacctat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggcttc tggcgaagg 850
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950
 tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcatttttag aaatatttca agaattatgg attgtgttgg 1350
 ttgttttaaa tgtcgtctgt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaactttt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
 1 5 10 15
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp
35 40 45

Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
50 55 60

Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg
65 70 75

Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp
80 85 90

Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln
95 100 105

Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr
110 115 120

Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu
125 130 135

Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys
140 145 150

Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe
155 160 165

Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp
170 175 180

Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp
185 190 195

Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys
200 205 210

Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln
215 220 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu
230 235 240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His
245 250 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu
260 265 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln
275 280 285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg
290 295 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu
305 310 315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465
Asn Ile His																	

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaaagacc tttaaactct ttggcttctg gtcaaggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct ttacaagag acctggtag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtgttacca ttcttngagc gcccagattt tcaactnttt 400
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500
tttgetg 507

<210> 339

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 339

aagctgccgg agctgcaatg 20

<210> 340

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 340

ttgcttctta atcctgagcg c 21

<210> 341

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

aaaggaggac tttcgactgc 20

<210> 342

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

agagattcat ccactgctcc aagtcg 26

<210> 343

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtgggta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggacttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatgat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggccca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agagggtggt ggcagtgtct ctgaaggtcc ataaaagaaa 550

aaagagaagt gtggtgaagg aaaatggtct gtgtggagg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactatth ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgcccgtg tggatgcttc 800

attccagcct caggaagcc tggcaccac tgccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
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gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150
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ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
1				5					10					15
Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
				20					25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
				35					40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
				50					55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
				65					70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
				80					85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
				95					100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
				110					115					120

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
cacagtcccc caccatcact cntcccatc cttccaactt tatttttagc 50
ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgtcct 200
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
gggggtggac agcgatggat gctggtgggc gcccctggg atgggccttc 350
aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500

tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttcgtcactc acctgttctt gcccctggtg ttcct 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggaggggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctcaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc aggggggagta cgagagcctg tacaogagcc acatctggat 500
ccccagcagc tgggtctcac tcaactgaagg tcctgagtgt gatgtcactg 550
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcaacaaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggagggagcc tggtgccgag gaacatgtca aaatgggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
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cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
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 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu
 1 5 10 15
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
 20 25 30

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50
cctttctagc ttcctggccg gctctagaac aattcaggct tcgctgcgac 100
tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250
tcatgtgggt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
tggatcccca gcagctgggtg ctcaactcact gaaggtcctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
agaaactcaa ccacccctac ccgacctggg atggagatca ccaaagatgg 650
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaacccttg cgcccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgctgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100

ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
tgagagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450
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ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550
gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
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agctcacatc ggaccagcac ctgacccga ggactggtgg agctacaagg 700

ataatctcca gggaaacttc gtgccagggc ctctttctg gggcctggtg 750
 aatgcagcgt ggagtctgtg tgctgtggg aagcggcaga gccccgtgga 800
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 catgtctcct tctgcctgc accccgacct gtggtcaatg tgtctggagg 950
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 ctgcgcagcg agcgggctcg gaacatcaga tcaaccacca gggcttctct 1050
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 cgctgcctcc cgcgggccca atggcctggc cattctcagc ctctttgtca 1150
 acgttgccag tacctctaac ccattcctca gtgcctcct taaccgcgac 1200
 accatcactc gcatctccta caagaatgat gcctactttc ttcaagacct 1250
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 gctctctcag caccocgccc tgctccgaga ctgtcacctg gatcctcatt 1350
 gaccgggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400
 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450
 ggcccctgca gcccttggcc cacagggcac tgaggggcaa cagggacccc 1500
 cggcaccocg agagggcgtg ccgaggcccc aactaccgcc tgcattgtga 1550
 tggtgtcccc catggctcgt gagactcccc ttcgaggatt gcaccgccc 1600
 gtcctaagcc tccccacaag gcgaggggag ttaccctaa aacaaagcta 1650
 ttaaagggac agaatactta 1670

<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
			20					25						30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
			35					40						45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
			50					55						60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
65 70 75

Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
80 85 90

Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
95 100 105

His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
110 115 120

Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
125 130 135

Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
140 145 150

His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
155 160 165

Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly
170 175 180

Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn
185 190 195

Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile
200 205 210

Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu
215 220 225

Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser
230 235 240

Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile
245 250 255

Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg
260 265 270

Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser
275 280 285

Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg
290 295 300

Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro
305 310 315

Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg
320 325

<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
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<210> 362
<211> 3038

<212> DNA
<213> Homo sapiens

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<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu			
				35					40					45			
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn			
				50					55					60			
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln			
				65					70					75			
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val			
				80					85					90			
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp			
				95					100					105			
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu			
				110					115					120			
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln			
				125					130					135			
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His			
				140					145					150			
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys			
				155					160					165			
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly			
				170					175					180			
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile			
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Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser			
				215					220					225			
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys			
				230					235					240			
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu			
				245					250					255			
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His			
				260					265					270			
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser			
				275					280					285			
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg			
				290					295					300			
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala			
				305					310					315			

Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr
320	325 330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile
335	340 345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg
350	355 360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile
365	370 375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr
380	385 390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro
395	400 405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg
410	415 420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr
425	430 435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His
440	445 450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro
455	460 465
Val Asp Lys Arg Lys Thr Tyr Ile Ala	Ser Phe Gln Asn Gly Ile
470	475 480
Phe Ser Glu Ser Leu Gln Asn Pro Pro	Gly Gly Lys Ala Phe Arg
485	490 495
Val Phe Ala Val Val	
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<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

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 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala
				20					25					30
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35					40					45
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50					55					60
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65					70					75
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80					85					90
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95					100					105
Arg	Arg	Val	Tyr	Glu	Glu									
				110										

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

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<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373
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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

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 gaagttttaa catttctttc tgtgccacac aatggatggc tctccttaag 2950
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<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150

Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser			
				155					160					165			
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu			
				170					175					180			
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly			
				185					190					195			
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly			
				200					205					210			
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu			
				215					220					225			
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly			
				230					235					240			
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly			
				245					250					255			
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser			
				260					265					270			
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu			
				275					280					285			
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile			
				290					295					300			
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met			
				305					310					315			
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln			
				320					325					330			
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile			
				335					340					345			
Asp	Gly	Asp	Val	Ile	Pro	Asp	Asp	Pro	Gln	Ile	Leu	Met	Glu	Gln			
				350					355					360			
Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Ile	Met	Leu	Gly	Val	Asn	Gln	Gly			
				365					370					375			
Glu	Gly	Leu	Lys	Phe	Val	Asp	Gly	Ile	Val	Asp	Asn	Glu	Asp	Gly			
				380					385					390			
Val	Thr	Pro	Asn	Asp	Phe	Asp	Phe	Ser	Val	Ser	Asn	Phe	Val	Asp			
				395					400					405			
Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Thr	Leu	Arg	Glu	Thr			
				410					415					420			
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Lys	Glu	Asn	Pro	Glu			
				425					430					435			

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	710	715	720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe
785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly
800 805 810

His Ser Thr Thr Arg Val
815

<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggaccctc tgggtcgtgg cagcagtggc 50
ggcgatgttt gtcggtcgg gatgggtcca ggatgttact ccttcttctt 100
ttgttggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150
cgagtacttg aaacgggagc actcgtgtc gaagccctac cagggtgtgg 200
gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250
accagtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300
gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg cagggtgcact 350
tcaaaatcca tggacaagga aagaagaatc tgcattggga tggcttggca 400
atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450
ggacaaatth gtggggctgg gagtatttgt agacacctac cccaatgagg 500
agaagcagca agagcgggta ttccctaca tctcagccat ggtgaacaac 550
ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600
aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttctggtga 650
ttcgctacgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700
catgagtgga gggactgcat tgaagtgcc ggagtccgcc tgccccgcgg 750

ctactacttc ggcacctcct ccactactgg ggatctctca gataatcatg 800
atgtcatttc cttgaagttg tttgaactga cagtggagag aaccccagaa 850
gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900
gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950
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ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350

caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400
 cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450
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 caaaagcaac atttgcctg tggtctgacc atgtggagat gtttctggac 1950
 ttgctagagc ctgcttagct gcatgttttg tagttacgat ttttggaaac 2000
 ccactttgag tgctgaaagt gtaaggaagc tttcttctta caccttgggc 2050
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 cttggagggc ctggaactct gagtcctcct atgaacctct gtagcctaaa 2350
 tgaaattctt aaaatcaccg atggaaccaa aaaaaaaaaa aaaaagggcg 2400
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 ggccgccatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg
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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20				25					30	

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly		35	40	45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro		50	55	60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met		65	70	75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp		80	85	90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe		95	100	105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln		110	115	120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr		125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys		140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu		155	160	165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn		170	175	180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr		185	190	195
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Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp		200	205	210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met		215	220	225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val		230	235	240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser		245	250	255
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys		260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu		275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro		290	295	300
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe		305	310	315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<210> 381
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
ccttgggtcg tggcagcagt gg 22

<210> 382
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
cactctccag gctgcatgct cagg 24

<210> 383
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
gtcaaacggt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
<211> 3150
<212> DNA
<213> Homo sapiens

<400> 384
ccgagccggg cgcgcagcga cggagctggg gccggcctgg gaccatgggc 50
gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100
ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
tggggctctgg ctccagaattc ctgcagctgg tgaaaatctg ttttctagaa 200

gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250
ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300
tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350
cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400
caagagtcga aagagaatca tgcccgaccc tgtgacggag cccctgtga 450
cagaccccg t tatgaagct cttttgtact gcaacatccc cagtgtggcc 500
gagcgcagca tggaagg tca tgccccgc at tttttaagc tggctctcagt 550
gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600
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cattgtgtga gatgggagag ctcacacaga caggagtgtg gcagcatttg 800
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gccggaccct acaaagtggg ctggccttgc tttatggctt tctccagat 950
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tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggacttt 1950
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tgtgatggaa ccagcacacc tcaacaaaaa tttttttaat cttagacatt 2100
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cctccagtaa cttctgctag aaacacagaa tttggtctgt atctgacact 2500
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gtgttgcat tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala
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Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile
20 25 30

Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys
35 40 45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro
50 55 60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu
65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser
80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
95 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala
110 115 120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His
125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu
155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu
170 175 180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp
185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr
200 205 210

Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe
215 220 225

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe
230 235 240

Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
				245					250					255	
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
				260					265					270	
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	
				275					280					285	
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	
				290					295					300	
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
				305					310					315	
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	
				320					325					330	
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
				335					340					345	
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	
				350					355					360	
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
				365					370					375	
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
				380					385					390	
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
				395					400					405	

Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
				410					415					420	
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
				425					430					435	
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
				440					445					450	
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
				455					460					465	
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	
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<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386
 ccaagcagct tagagctcca gacc 24

<210> 387
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 387
 ttccctatgc tctgtattgg catgg 25

<210> 388
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 388
 gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
 <211> 3313
 <212> DNA
 <213> Homo sapiens

<400> 389
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cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100
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 gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200
 cacgcgcctg aagcaciaag cagatagcta ggaatgaacc atccctggga 250
 gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300
 gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350
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 atgcacccag atacgctatt cagttccgga agagctggag aaaggctcta 500
 ggggtgggca catctccagg gacctggggc tggagccccg ggagctcgcg 550
 gagegcggag tccgcatcat cccagaggt aggacgcagc ttttcgcctt 600
 gaatccgcgc agcggcagct tggtcacggc gggcaggata gaccgggagg 650

agctctgtat gggggccatc aagtgtcaat taaatctaga cattctgatg 700
gaggataaag tgaaaatata tggagtagaa gtagaagtaa gggacattaa 750
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<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly
575 580 585

Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln
590 595 600

Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly
605 610 615

Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg
620 625 630

Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala
635 640 645

Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu
650 655 660

Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu
665 670 675

Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr
680 685 690

Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu
695 700 705

Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His
710 715 720

Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala
725 730 735

Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu
740 745 750

Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys
755 760 765

Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val
770 775 780

Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly
785 790 795

Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser
800 805 810

Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser
815 820 825

Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln
830 835 840

Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn
845 850 855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu
875 880 885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccaggtaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcacatggg acgccccga cctcgtgagg ccaagacgtg 200
 gatgttcttg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
 aggaggacaa ggtgctgggg ggtcatgagt gccaaaccca ttcgcagcct 300
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 caagaaatac ctgtggttca gtccatccca caccctgct acaacagcag 500
 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
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ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15

Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
				35					40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
				50					55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn
80 85 90

Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro
95 100 105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp
110 115 120

Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys
125 130 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln
140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu
155 160 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro
170 175 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly
185 190 195

Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly
230 235 240

Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile
245 250 255

Ile Gly Ser Lys Gly
260

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccggccc gccgcgccgc ccacgcccc accccggccc gcgcccccta 100

gccccgccc gggcccgcg ccgcgcccgc gccaggtga gcgctccgcc 150

cgccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcatectccc ggcgccccgc gctgcgagcg ccccgccagt ccgcgccgcc 300

gccgcctctg cctgtgcgc cctgcgcgcc ctgcgcaccc ggggcccag 350

cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400

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gggagacggg cgcgcgcccc gaaacgactt tcagtcccc acgcgccccg 500

cccaaccctt acgatgaaga gggcgtccgc tggaggagc cggtgctgg 550

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 ttacagggtt cggcggcagc gtttgttcca gaacgccgc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20						25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
				50					55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
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Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val
275 280 285

Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg
290 295 300

Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro
305 310 315

Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu
320 325 330

Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser
335 340 345

Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys
350 355 360

Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly
365 370 375

Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser
380 385 390

Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro
395 400 405

Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser
410 415 420

Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly
425 430 435

Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu
440 445 450

Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val
455 460 465

Leu Trp Thr Val Leu Gly Pro Cys
470

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50

ggagaggact actcactggc atattttctga ggtatctgta gaataaccac 100

agcctcagat actgggggact ttacagtccc acagaaccgt cctcccagga 150

agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350

tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ctttcgagtt ttttcaagct gagctgcaag taatagacat 550

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<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405

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Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu
			20						25					30

Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
				35					40					45
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50						55					60
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65						70					75
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys
			80						85					90
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95						100					105
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala
			110						115					120
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125						130					135
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140						145					150

Thr	Thr	Phe	Pro	Leu	Lys	Asn	Ala	Glu	Asp	Leu	Asp	Val	Gly	Gln	
				155					160					165	
Asn	Asn	Ile	Glu	Asn	Tyr	Ile	Ile	Ser	Pro	Asn	Ser	Tyr	Phe	Arg	
				170					175					180	
Val	Leu	Thr	Arg	Lys	Arg	Ser	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu	
				185					190					195	
Val	Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Glu	Ala	Glu	Leu	Arg	
				200					205					210	
Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	
				215					220					225	
Thr	Ala	Gln	Val	Tyr	Ile	Glu	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	
				230					235					240	
Pro	Glu	Phe	Glu	Gln	Pro	Phe	Tyr	Arg	Val	Gln	Ile	Ser	Glu	Asp	
				245					250					255	
Ser	Pro	Val	Gly	Phe	Leu	Val	Val	Lys	Val	Ser	Ala	Thr	Asp	Val	
				260					265					270	
Asp	Thr	Gly	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Ser	Leu	Phe	Gln	Ala	
				275					280					285	
Ser	Glu	Glu	Ile	Gly	Lys	Thr	Phe	Lys	Ile	Asn	Pro	Leu	Thr	Gly	
				290					295					300	
Glu	Ile	Glu	Leu	Lys	Lys	Gln	Leu	Asp	Phe	Glu	Lys	Leu	Gln	Ser	
				305					310					315	
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Tyr	Glu	Val	Asn	Ile	Glu	Ala	Arg	Asp	Ala	Gly	Thr	Phe	Ser	Gly	
				320					325					330	
Lys	Cys	Thr	Val	Leu	Ile	Gln	Val	Ile	Asp	Val	Asn	Asp	His	Ala	
				335					340					345	
Pro	Glu	Val	Thr	Met	Ser	Ala	Phe	Thr	Ser	Pro	Ile	Pro	Glu	Asn	
				350					355					360	
Ala	Pro	Glu	Thr	Val	Val	Ala	Leu	Phe	Ser	Val	Ser	Asp	Leu	Asp	
				365					370					375	
Ser	Gly	Glu	Asn	Gly	Lys	Ile	Ser	Cys	Ser	Ile	Gln	Glu	Asp	Leu	
				380					385					390	
Pro	Phe	Leu	Leu	Lys	Ser	Ala	Glu	Asn	Phe	Tyr	Thr	Leu	Leu	Thr	
				395					400					405	
Glu	Arg	Pro	Leu	Asp	Arg	Glu	Ser	Arg	Ala	Glu	Tyr	Asn	Ile	Thr	
				410					415					420	
Ile	Thr	Val	Thr	Asp	Leu	Gly	Thr	Pro	Met	Leu	Ile	Thr	Gln	Leu	
				425					430					435	

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440		445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455		460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470		475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485		490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500		505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515		520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530		535	540
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545		550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560		565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575		580	585
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590		595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605		610	615
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620		625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635		640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650		655	660
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665		670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680		685	690
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695		700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710		715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgtca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgtct cattcaggag gatctaccct tctctctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 cggtcgacga ccgccccgcg tcatgoggct cctcggttg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
 agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
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 gatcacatgg tgatgtgtc tgtgattcct ggggaagctg aggacaaagt 400
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 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500
 cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550
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<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

Met	Val	Pro	Ala	Ala	Gly	Arg	Arg	Pro	Pro	Arg	Val	Met	Arg	Leu
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Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val
				20					25					30
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
				80					85					90
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
				155					160					165
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly

260					265					270				
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu
				275					280					285
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys
				290					295					300
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro
				305					310					315
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu
				320					325					330
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu
				335					340					345
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu
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<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgg cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

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<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150
gcgcagcaat tgcaagccca tcccgggtcaa cctgcagctg tgccacggca 200
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accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcggg 750
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gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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20		25	30
Pro Asp Phe Ser Tyr	Lys Arg Ser Asn Cys	Lys Pro Ile Pro Val	
35		40	45
Asn Leu Gln Leu Cys	His Gly Ile Glu Tyr	Gln Asn Met Arg Leu	
50		55	60
Pro Asn Leu Leu Gly	His Glu Thr Met Lys	Glu Val Leu Glu Gln	
65		70	75
Ala Gly Ala Trp Ile	Pro Leu Val Met Lys	Gln Cys His Pro Asp	
80		85	90
Thr Lys Lys Phe Leu	Cys Ser Leu Phe Ala	Pro Val Cys Leu Asp	
95		100	105
Asp Leu Asp Glu Thr	Ile Gln Pro Cys His	Ser Leu Cys Val Gln	
110		115	120
Val Lys Asp Arg Cys	Ala Pro Val Met Ser	Ala Phe Gly Phe Pro	
125		130	135
Trp Pro Asp Met Leu	Glu Cys Asp Arg Phe	Pro Gln Asp Asn Asp	
140		145	150
Leu Cys Ile Pro Leu	Ala Ser Ser Asp His	Leu Leu Pro Ala Thr	
155		160	165
Glu Glu Ala Pro Lys	Val Cys Glu Ala Cys	Lys Asn Lys Asn Asp	
170		175	180
Asp Asp Asn Asp Ile	Met Glu Thr Leu Cys	Lys Asn Asp Phe Ala	
185		190	195
Leu Lys Ile Lys Val	Lys Glu Ile Thr Tyr	Ile Asn Arg Asp Thr	
200		205	210
Lys Ile Ile Leu Glu	Thr Lys Ser Lys Thr	Ile Tyr Lys Leu Asn	
215		220	225
Gly Val Ser Glu Arg	Asp Leu Lys Lys Ser	Val Leu Trp Leu Lys	
230		235	240
Asp Ser Leu Gln Cys	Thr Cys Glu Glu Met	Asn Asp Ile Asn Ala	
245		250	255
Pro Tyr Leu Val Met	Gly Gln Lys Gln Gly	Gly Glu Leu Val Ile	
260		265	270
Thr Ser Val Lys Arg	Trp Gln Lys Gly Gln	Arg Glu Phe Lys Arg	
275		280	285
Ile Ser Arg Ser Ile	Arg Lys Leu Gln Cys		

<210> 416
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 418
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<210> 419
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<400> 419
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 ccgagccccg ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100
 cgctgggtgt tcctgtctgc gatcagcctg ctcaactgct ccaacgccac 150
 gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
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 <212> PRT
 <213> Homo sapiens

<400> 420

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Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp
				20					25					30

Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45

Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60

Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75

Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90

Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105

Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val
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Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu
				125					130					135

Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu
				140					145					150

Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met
				155					160					165

Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val
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Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met
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Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser
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Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala
				215					220					225

Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys
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Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys
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Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu
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Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly
275 280 285

Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu
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Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala
305 310 315

Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe
320 325 330

Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala
335 340 345

Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val
350 355 360

Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly
365 370 375

Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile
380 385 390

Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu
395 400 405

Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr
515 520 525

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Pro Trp Val Ile Thr
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<400> 422
cggttcaata aacctggacg cttgg 25

<210> 423
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<210> 424
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 <212> PRT
 <213> Homo sapiens

<400> 425
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Gly Tyr Leu Phe	Leu Leu Gly Asp Cys	Gln Glu Val Thr Thr Leu	20	25	30
Thr Val Lys Tyr	Gln Val Ser Glu Glu Val	Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly Arg	Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala	Ala Phe Gln Val Leu Gln	Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val	Asp Ser Glu Glu Gly Leu	Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg	Glu Gln Leu Cys Arg Gln	Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp	Val Leu Ala Thr Gly Asp	Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln	Val Leu Asp Ile Asn Asp	His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu	Gln Glu Leu Glu Ile Ser	Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile	Pro Leu Asp Arg Ala Leu	Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu	His Thr Tyr Thr Leu Ser	Pro Ser Glu His Phe	170	175	180

Ala Leu Asp Val	Ile Val Gly Pro Asp Glu	Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val	Lys Glu Leu Asp Arg Glu	Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn Gly	Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val Leu	Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu Ala	Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile Lys	Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val Glu	Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr Phe	Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn
305 310 315

Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn
320 325 330

Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val
335 340 345

Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro
350 355 360

Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu
365 370 375

Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His
380 385 390

Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr
395 400 405

Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg
410 415 420

Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln
425 430 435

Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile
440 445 450

Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr
455 460 465

Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile
470 475 480

Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val
485 490 495

Ser Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile
500 505 510

Asp Ser Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr
515 520 525

Glu Glu Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser
530 535 540

Gly Gln Pro Met Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu
545 550 555

Leu Asp Ala Asn Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu
560 565 570

Ser Asp Gly Lys Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr
575 580 585

Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
590		595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
605		610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
620		625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
635		640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn	Val
650		655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
665		670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
680		685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp	Ser
695		700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
710		715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
725		730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
740		745	750

Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
755		760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro	Val
770		775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

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<213> Artificial Sequence

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<210> 427

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<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

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<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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 tttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
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 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
 35 40 45
 Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
 50 55 60
 Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
 65 70 75
 Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
 80 85 90
 Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
 95 100 105
 His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
 110 115 120
 Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser
 125 130 135
 Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val
 140 145 150
 Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly
 155 160 165
 Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn
 170 175 180
 Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln

	185	190	195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
	215	220	225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
	425	430	435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
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Lys Gln Met Ala	Pro		
	455		

<210> 431

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

<400> 431
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ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
gagctcatca tctttgaaat cttnngagta ttgaatagca gctcccgta 250
ttttcactgg aaaatgaacc tgtgtgtaat tctgctgac ctggttntca 300
tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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tatttttttg atttgggta gnttttttc atgcgccaat tgtttaaaga 150
ctatgagata cgtcagtatg ttgtacaggt gatntntcc gtgacgtttg 200
catttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
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tctgctgac ctggttttca tggtgccttt ttacattggc tattttattg 350
tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgttttaa gactatgaga tacgtcagta tgtgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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ttctcacggg ctgtcgctt caatctggac gtgatgggtg ccttgcgcaa 150

ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgaccccag agctggctgc tgggtgggtgc tccccaggcc 250

ctggctcttc ctgggcagca ggcgaatgc actggaggcc tcttcgcttg 300

cccgttgagc ctggaggaga ctgactgcta cagagtggac atcgaccagg 350

gagctgatat gcaaaaggaa agcaaggaga accagtgggtt gggagtcagt 400

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 ttcgtctatt tattaataaaa tatttgagaa caaaaaaaaaa aaaaaaaaaa 3950
 a 3951

<210> 437
 <211> 1141
 <212> PRT
 <213> Homo sapiens

<400> 437
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 Cys Tyr Leu Phe Gly Ser Leu Leu Val Glu Leu Leu Phe Ser Arg
 20 25 30
 Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu
 35 40 45
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
 50 55 60
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
 65 70 75
 Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly
 80 85 90
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg
 95 100 105

Val Asp Ile Asp	Gln Gly Ala Asp	Met Gln Lys Glu Ser Lys	Glu
110		115	120
Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly	Gly
125		130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg	Val
140		145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe	Val
155		160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly	Glu
170		175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe	Gly
185		190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser	His
200		205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly	Thr
215		220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala	His
230		235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln	Asp
245		250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe	Ser
260		265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser	Phe
275		280	285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val	Ile
290		295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met	Leu
305		310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala	Val
320		325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly	Ala
335		340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val	Tyr
350		355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro	Leu
365		370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu	Ala
380		385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly
680		685 690
Leu Glu Leu Met Val	Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro	
695		700 705
Gln Ala Asp Gly Asp	Asp Ala His Glu Ala Gln Leu Leu Val Met	
710		715 720
Leu Pro Asp Ser Leu	His Tyr Ser Gly Val Arg Ala Leu Asp Pro	
725		730 735
Ala Glu Lys Pro Leu	Cys Leu Ser Asn Glu Asn Ala Ser His Val	
740		745 750
Glu Cys Glu Leu Gly	Asn Pro Met Lys Arg Gly Ala Gln Val Thr	
755		760 765
Phe Tyr Leu Ile Leu	Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr	
770		775 780
Glu Leu Glu Val Glu	Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu	
785		790 795
Leu His Pro Val Ser	Ala Arg Ala Arg Val Phe Ile Glu Leu Pro	
800		805 810
Leu Ser Ile Ala Gly	Met Ala Ile Pro Gln Gln Leu Phe Phe Ser	
815		820 825
Gly Val Val Arg Gly	Glu Arg Ala Met Gln Ser Glu Arg Asp Val	
830		835 840
Gly Ser Lys Val Lys	Tyr Glu Val Thr Val Ser Asn Gln Gly Gln	
845		850 855
Ser Leu Arg Thr Leu	Gly Ser Ala Phe Leu Asn Ile Met Trp Pro	
860		865 870
His Glu Ile Ala Asn	Gly Lys Trp Leu Leu Tyr Pro Met Gln Val	
875		880 885
Glu Leu Glu Gly Gly	Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser	
890		895 900
Pro Arg Pro Asn Ile	Leu His Leu Asp Val Asp Ser Arg Asp Arg	
905		910 915
Arg Arg Arg Glu Leu	Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu	
920		925 930
Arg Gln Glu Pro Ser	Met Ser Trp Trp Pro Val Ser Ser Ala Glu	
935		940 945
Lys Lys Lys Asn Ile	Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn	
950		955 960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccaaga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcga gcacagtgcg ggctcacaac aagatgctca aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcggcggt ggctgcagcc gggggcggt cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

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aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtgggtcta tcccagccct gtttgtggtt cagatggtca 600

tacctactct tttcagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttcagataag 700

cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750

caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950
 tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000
 aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050
 ctactgcttc cagagacagc aagaccacc ttgccagact gagctcagca 1100
 atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150
 ctgtgtgatg aagatggtta ctacaagcca acacaatgtc atggcagtgt 1200
 tggacagtgc tgggtgtgtg acagatatgg aatgaagtc atgggatcca 1250
 gaataaatgg tgttcagat tgtgctatag attttgagat ctccggagat 1300
 tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350
 cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400
 gggatgatga tgatgggtgg gatgaccatg atgtatacat ttgattgatg 1450
 acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500
 cctattttaa attatcttct tcccaataa caaatgatt ctaaacctca 1550
 catatatttt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600
 ttatgtttaa ataagaatca tttgctttga gtttttatat tccttacaca 1650
 aaaagaaaat acatatgcag tctagtcaga caaaataaag ttttgaagtg 1700
 ctactataat aaatttttca cgagaacaaa ctttgtaaat cttccataag 1750
 caaatgaca gctagtgctt gggatcgtac atgttaattt tttgaaagat 1800
 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442
 <211> 436
 <212> PRT
 <213> Homo sapiens

<400> 442
 Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp
 1 5 10 15
 Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly
 20 25 30
 Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35					40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys
				50					55					60
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro
				65					70					75
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys
				80					85					90
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp
				95					100					105
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg
				110					115					120
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile
				125					130					135
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val
				140					145					150
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu
				155					160					165
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu
				170					175					180
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg
				185					190					195
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala
				200					205					210
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser
				215					220					225
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg
				230					235					240
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp
				245					250					255
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln
				260					265					270
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr
				275					280					285
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile
				290					295					300
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro
				305					310					315
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val

320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro	Leu Cys Asp Glu Asp Gly	
335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly	Ser Val Gly Gln Cys Trp	
350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val	Met Gly Ser Arg Ile Asn	
365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe	Glu Ile Ser Gly Asp Phe	
380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr	Asp Asp Glu Asp Asp Glu	
395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu	Ile Glu Asp Asp Asp Glu	
410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly	Asp Asp His Asp Val Tyr	
425	430	435

Ile

<210> 443
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
 cagcaatatt cagaagcggc aaggg 25

<210> 444
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 catcatggtc atcaccacca tcatcatc 28

<210> 445
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

cagactccag atttcctgt caaccacgag gagtccagag aggaaacgcg 50

gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100

cagggatggg cgacaagatc tggctgccct tccccgtgct ccttctggcc 150

gctctgcctc cgggtgctgct gcctggggcg gccgggttca caccttcct 200

cgatagcgac ttcaccttta cccttcccgc cggccagaag gagtgcttct 250

accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagtttta 300

gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350

aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400

ctgaagttgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450

tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500

ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550

tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600

agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650

tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700

ctatgggtaa tttagtggtc atggtgggtg tgtcagccat tcaagtttat 750

atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaaactc 800

caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850

tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900

aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950

tgtgcaagta atcctgctga tccagttgta ctttaagtgtg taacaggaat 1000

attttgca atagagttt aactgaatga agccatatta ataactgcat 1050

tttcctaact ttgaaaaatt ttgcaaagt cttaggtgat ttaaataaat 1100

gagtattggg cctaattgca acaccagtct gtttttaaca gggttctatta 1150

cccagaactt ttttgtaaat gcggcagtta caaattaact gtggaagttt 1200

tcagttttta gttataaatc acctgagaat tacctaataa tggattgaat 1250

aaatcttttag actacaaaag cccaactttt ctctattttac atatgcatct 1300
ctcctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350
agatttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400
tagtctttgt actttgctta cattcccaa agctgacatt ttcacgattc 1450
ttaaaaacac aaagttacac ttactaaaat taggacatgt tttctctttg 1500
aatgaagaa tatagtttaa aagcttcctc ctccataggg acacattttc 1550
tctaaccctt aactaaagt taggatttta aaattaaatg tgaggtaaaa 1600
taagtttatt tttaatagta tctgtcaagt taatatctgt caacagttaa 1650
taatcatgtt atgttaattt taacatgatt gctgacttgg ataattcatt 1700
attaccagca gttatgaagg aaatattgct aaaatgatct gggcctacca 1750
taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800
agaatttaga aaaacttgag aaaacctaat ccaaaaataa attcacttaa 1850
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900
tactcataac ataaatcaaa ggagatgatt aatttcagt tagctggaag 1950
aaactttggc tgtaggtttt tattttctac agaattctg gtttgaatta 2000
ttttgtaag caggtagatt ttataaaatg taagccctac tgtaaggttt 2050

agcactgggt gtacatattt attaaaaatt tttattataa caacttttat 2100
taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150
gaaacataga ctcccaagtt ttaaacacct aaatgtgaat aacctatata 2200
tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250
tcaagtacta gtaatttaac ttcattcatga atgaactata atttttaagt 2300
tatgcccatt tataacgttg tttatgacta cattgtgagt tagaaacaaa 2350
cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400
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cttagatttc octactggca aggtttttta aaatgaggta aatgccgtat 2550
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 tataaaaactg tgattaagaa ttctacctct cctgtatggc tgttactgta 2800
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 acatgtatga tttgtgccac tgatcttaaa cctatgattc agtaacttct 2900
 taccatataa aaacgataat tgctttatct ggaaaagaat ttaggaatac 2950
 taaggacaat tatttttata gacaaagtaa aaagacagat atttaagagg 3000
 cataacccaaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatatct 3050
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 aacagctcat tttgtctttt tcaatatata aatttttaaaa atactacaat 3200
 atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250
 cctcacacta aggcctagag tttgctctga tatgcatttg gatgattaat 3300
 gttatgctgt tctttcatgt gaatgtcaag acatggaggg tgtttgtaat 3350
 tttatggtaa aattaatcct tcttacacat aatgggtgtct taaaattgac 3400
 aaaaaatgag cacttacaat tgtatgtctc ctcaaagaa gattctttat 3450
 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcattctgaa 3500
 gtacaataat gcacaatcag tgttgcctca actgctttat acttataaac 3550
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 447
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala
 1 5 10 15
 Ala Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro
 20 25 30
 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys
 35 40 45
 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile
 50 55 60

Glu Tyr Gln Val	Leu Asp Gly Ala Gly	Leu Asp Ile Asp Phe His
65	70	75
Leu Ala Ser Pro	Glu Gly Lys Thr Leu Val	Phe Glu Gln Arg Lys
80	85	90
Ser Asp Gly Val	His Thr Val Glu Thr	Glu Val Gly Asp Tyr Met
95	100	105
Phe Cys Phe Asp	Asn Thr Phe Ser Thr	Ile Ser Glu Lys Val Ile
110	115	120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln Glu
125	130	135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu Asp
140	145	150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys Ser
155	160	165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala Phe
170	175	180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg Val
185	190	195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val Ser
200	205	210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys Arg
215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50

agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100

gccctgccca gtgtgtcctg gatgctgctt tcttgctca ttctcctgtg 150

tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200

gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250

ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350

~~cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400~~

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccttgccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

ttctcccaa actgccctac ctgactacct tgtcatgac ctccttcttt 750

ttcctttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800

gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850

aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT
<213> Homo sapiens

<400> 452

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu
1 5 10 15

Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln
20 25 30

Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
35 40 45

Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser
50 55 60

Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys
65 70 75

Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser
80 85 90

Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly
95 100 105

Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp
110 115 120

Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys
125 130 135

Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser
140 145 150

Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala
155 160 165

Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp
170 175

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

ccagtctgtc gccacctcac ttggtgtctg ctgtccccgc caggcaagcc 50

tggggtgaga gcacagagga gtgggcccgg accatgcggg ggacgcggct 100

ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150

tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200

atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250

ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
 tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450
 tccgactgta gagtccccgc ccacccccat ggcctatgc ggcccagccc 500
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454

<211> 125

<212> PRT

<213> Homo sapiens

<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala
 1 5 10 15

Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
 20 25 30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
 35 40 45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
 50 55 60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
 65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
 80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
 95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
 110 115 120

Leu Ser Leu Arg Leu
 125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

ctgcagtcag gactctggga ccgcaggggg ctcccggacc ctgactctgc 50

agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100

atcttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150

gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
 ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300
 acccaggctc tgcagtcagc gccgcgcggg gaatcctgta cccgggcggg 350
 aataagtacc agaccattga caactaccag ccgtaccggt gcgcagagga 400
 cgaggagtgc ggactgatg agtactgcgc tagtcccacc cgcggagggg 450
 acgcaggcgt gcaaattctgt ctgcctgca ggaagcgccg aaaacgctgc 500
 atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
 ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750
 tctggtccaa gatctgtaaa cctgtcctga aagaaggta agtgtgtacc 800
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttgta 850
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
 ctttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
 gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100
 ttatggaact cccctgtgat tgcagtaaat tactgtattg taaattctca 1150
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200
 ggtgctgcac tgcctatttt tcctcttggt atgtaaattt ttgtacacat 1250
 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaatca 1300
 tttcagctta tagttcttaa aagcataacc ctttacccca tttaattcta 1350
 gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
 ttaaattata ttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500
 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT
<213> Homo sapiens

<400> 456

Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala
1 5 10 15

Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser
20 25 30

Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu
35 40 45

Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val
50 55 60

Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln
65 70 75

Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu
80 85 90

Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp
95 100 105

Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg
110 115 120

Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn
125 130 135

Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile
140 145 150

Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu
155 160 165

Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His
170 175 180

Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys
185 190 195

Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys
200 205 210

Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg
215 220 225

Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser
245 250 255

Asn Ser Ser Arg Leu His Thr Cys Gln Arg His
260 265

<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
509, 556
<223> unknown base

<400> 457
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gcgcagcggg agctaaccgc gttttttgtg gcgatggtag cggcgggttt 200
cggcggccac ctntgtctgg gagtgcgcgc caccttgaat cggttttcaa 250
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<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

<400> 458
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ttctctcctg cacgcggtgc ttgggctcgg ccaggcgggg tccgccgcca 150
gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200
gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250
ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcacct 300

tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350
accagcagtg aatcttaatg ttcaacttaaa tcagaacttg cataagaaag 400
agaatgggag tctgggttaaa taaagatgac tatatcagag acttgaaaag 450
gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500
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cattggaaag aagagaatgt gatgctgctg ttaattctgg agaactgtgg 850
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ggctcatcat cggtaggtgt tattttttca ttttgaaaaa aatgaaaatt 1400
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attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys
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Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu
80 85 90

Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu
95 100 105

Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr
110 115 120

Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu
125 130 135

Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe
140 145 150

Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala
155 160 165

Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg
170 175 180

Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met
185 190 195

Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly
200 205 210

Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu
215 220 225

Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu
230 235 240

~~Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala~~
245 250 255

Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys
260 265 270

Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu
275 280 285

Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn
290 295 300

Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg
305 310 315

Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn
320 325 330

Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu
335 340 345

Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala
350 355 360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
				665					670					675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
				725					730					735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu			
				740					745					

<210> 460
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 460
 actccccagg ctgttcacac tgcc 24

<210> 461
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 461
 gatcagccag ccaataccag cagc 24

<210> 462
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 462
 gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 463

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caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
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aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgac 450
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cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700
aacctcatgt ctctgccag tttttgtgaa tactgggttc accaaaaatc 750

caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800
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 atggacccaa gagaagaa 1818

<210> 464
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 464
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 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg
 20 25 30
 Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
 35 40 45
 His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln
 50 55 60
 Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu
 65 70 75
 Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr
 80 85 90
 Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn
 95 100 105
 Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn
 110 115 120
 Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu
 125 130 135
 Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp
 140 145 150
 Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro		
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe		
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly		
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe		
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp		
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys		
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln		
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln		
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys		
290	295	300

<210> 465
 <211> 1547
 <212> DNA
 <213> Homo sapiens

<400> 465
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 gagagggccc agcccggccg gggcaggatg accaaggccc ggctgttccg 150
 gctgtggctg gtgctggggt cgggtgttcat gatcctgctg atcatcgtgt 200
 actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250
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 cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450
 gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500
 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550

aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600
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gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700
cgcggtgcgc cctaccgca cccgctgcgc atcccgcgcg agcacgtgca 750
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agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850
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gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500
atcgatatgt ttttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
				20					25					30
Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
				35					40					45
Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
				50					55					60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu
335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp
410

<210> 467

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

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gggggcgggc ggggcatcgg agctgggacg gtgcgcgcct tcgtgaacag 200

cgggggccga gtggttatct gcgacaagga tgagtctggg ggccgggccc 250

tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300

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cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

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cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600

aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650

ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700

tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750

ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttcttggc 800

ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850

cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

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 ccataaaaac gatttgcagc c 1071

<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468

Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr
 1 5 10 15

Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val
 20 25 30

Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
 35 40 45

Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
 50 55 60

Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
 65 70 75

Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
 80 85 90

Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
 95 100 105

Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
 110 115 120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn
 125 130 135

Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln
 140 145 150

Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr
 155 160 165

Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn
 170 175 180

Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu
 185 190 195

Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met
 200 205 210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
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 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300
 acttgcatgt gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400

gtgccttgtt ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450
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 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
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<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 470
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 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

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				35					40					45
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50					55					60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
				110					115					120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
				155					160					165
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
				170					175					180

<210> 471

<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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ctccccgccg agaagcctcg ctcggcgcc aacatggcgg gtgggcgctg 150

cggcccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200

cgacggcagg ccccaggag gccgcgctgc cgccggagca gagccgggtc 250

cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300

gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350

aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400

aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450

cactctccca gcattttttc atgcaaagga tgggatattc cgccgttattc 500

gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
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gtaccaaatc cttaattttt cctgaatgag caagcttctc ttaaaagatg 1300
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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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Ala	Trp	Ile	Ala	Ala	Val	Ala	Ala	Thr	Ala	Gly	Pro	Glu	Glu	Ala
			20						25					30

Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
				35					40					45

Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
				50					55					60

Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
				65					70					75

Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
				80					85					90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105

Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120

Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135

Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150

Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165

Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr	170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr	Val Phe Phe Val Ile Ala	185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile	200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg	215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln	230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu	245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu	Glu Glu Lys Glu Asp Leu	260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu	Glu Glu Glu Asp Asn Leu	275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Glu Ala Asn Asp Gln Gly	290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Glu Glu Val Glu Pro Glu	305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr	320	325	330

Glu Val Val Glu	Asp Ser Leu Arg Gln	Arg Lys Ser Gln His Ala	335	340	345
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Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgaccgctc caac 24

<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

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Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val
 20 25 30

Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
 35 40 45

Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60

Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75

Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90

Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105

Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120

Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135

Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150

Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165

Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
 170 175 180

Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
 185 190 195

Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
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<210> 479
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
acaagtgtct tcccaacctg 20

<210> 480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
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<210> 481
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 482
<211> 3819
<212> DNA
<213> Homo sapiens

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ccgtcggagg aaaatgactc ccagtcgct gctgcagacg aactgttcc 250
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 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe
 80 85 90

Cys Leu Tyr Trp Asn Arg His Ala Gly Arg Leu His Leu Leu Tyr
95 100 105

Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala Ser Ser Leu Leu
110 115 120

Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly Pro Pro Leu
125 130 135

Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn Ile Ser
140 145 150

Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro Pro
155 160 165

His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys
170 175 180

Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys
185 190 195

Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln
200 205 210

Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met
215 220 225

Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu
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Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln
245 250 255

Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro
260 265 270

Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu
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Lys Arg Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln
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Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile
305 310 315

Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val
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Leu Thr Phe Gln His Gln Leu Gln Pro Lys Asn Val Thr Leu Gln
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Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His
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Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr
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Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val
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Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val
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Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg
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Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu
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Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile
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Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu
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Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr
500 505 510

Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly
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Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp
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Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly
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Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser
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Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn
575 580 585

Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg
590 595 600

Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu
605 610 615

Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe
620 625 630

Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile
635 640 645

Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser
650 655 660

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Ser Arg Ile

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<213> Homo sapiens

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<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

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<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

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<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

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<223> unknown base

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<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
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His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
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Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
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Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
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Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
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Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
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Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
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Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
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Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
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Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180
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Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	200	205	210
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	215	220	225
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	230	235	240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	245	250	255
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	260	265	270
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	275	280	285
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	290	295	300
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	305	310	315
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	320	325	330

His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	335	340	345
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<223> Synthetic oligonucleotide probe

<400> 489

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<211> 20

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 491

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<212> DNA

<213> Homo sapiens

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 Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn
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 His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro
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 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn
 65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His
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 Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu
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 Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro
 110 115 120
 Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp
 125 130 135
 Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu
 140 145 150
 Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys
 155 160 165
 Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
 170 175 180
 Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile
 185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp
245 250 255

Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys
260 265 270

Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala
275 280 285

Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn
290 295 300

Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys
305 310 315

Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile
320 325 330

Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu
335 340 345

Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met
350 355 360

Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu
365 370 375

Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu
380 385 390

Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly
395 400 405

Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe
410 415 420

Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro
425 430 435

Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr
440 445 450

Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr
455 460 465

Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
470 475 480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly
485 490 495

Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser
500 505 510

Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser
515 520 525

Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro
530 535 540

Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp
545 550 555

Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val
560 565 570

Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile
575 580 585

Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys
590 595 600

Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr
605 610 615

Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His
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Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu
635 640 645

Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn
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Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro
665 670 675

Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe
680 685 690

Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp
695 700 705

Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn
710 715 720

Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile
725 730 735

Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg
740 745 750

Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr
755 760 765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu
770 775 780

His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val
785 790 795

Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr
800 805 810

Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val
815 820 825

Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu
830 835 840

Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val
845 850 855

Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile
860 865 870

Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile
875 880 885

Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys
890 895 900

Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys
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Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu
920 925 930

Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln
935 940 945

Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
950 955 960

Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His
965 970 975

Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe
980 985 990

Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys
995 1000 1005

Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln
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Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr
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<212> PRT
<213> Homo sapiens

<400> 498

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Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr
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Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile
65 70 75

Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr
80 85 90

Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly
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Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala
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Phe Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn
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Gln Leu Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu
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Leu Ser Leu Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly
155 160 165

Ile Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn
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Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly
185 190 195

Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe
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Asn Ser Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg
215 220 225

Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu
230 235 240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly
245 250 255

Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys
260 265 270

Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn
275 280 285

Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg
290 295 300

Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val
305 310 315

Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly
320 325 330

Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser
335 340 345

Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser
350 355 360

Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg
365 370 375

Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu
380 385 390

Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe
395 400 405

Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu
410 415 420

Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys
425 430 435

Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His
440 445 450

Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser
455 460 465

Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala
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Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe
485 490 495

Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu
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Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu
515 520 525

Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn
530 535 540

Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp
545 550 555

Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile
560 565 570

Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn
575 580 585

Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr
590 595 600

Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe
605 610 615

Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg
620 625 630

Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp
635 640 645

Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu
650 655 660

Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met
665 670 675

Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu
680 685 690

Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp
695 700 705

Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser
710 715 720

His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val
725 730 735

Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr
740 745 750

Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser
755 760 765

Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile
770 775 780

Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile
785 790 795

Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg
800 805 810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp
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Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr
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Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp
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Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr
860 865 870

Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser
875 880 885

Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
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Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu
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Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp
920 925 930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val
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Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe
950 955 960

Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile
965 970 975

Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
980 985 990

Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro
995 1000 1005

Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn
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Asp Ser Ile Lys Gln Tyr
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 gctgggtggg gcctcagtgg gggctgctgc ctgaccccca gcacaataaa 1600
 aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
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 gcccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 506

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
 20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
 110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
 140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu

	155		160		165
Gly His Ser Leu	Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly		
	170		175		180
Gly Pro Pro Arg	Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala		
	185		190		195
Met Lys Glu Glu	Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu		
	200		205		210
Glu Glu Lys Leu	Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala		
	215		220		225
Ser Gln Ala Leu	Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu		
	230		235		240
Val His Ser Phe	Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu		
	245		250		255
Gln Ile Ser Phe	Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys		
	260		265		270

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507
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 cgccctgcgg tgtcccgagg gctgaggtct cctcatcttc tccctagcag 250
 tggatgagca acccaacggg ggcccgggga ggggaactgg ccccgaggga 300
 gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350
 gcagcccccga ggaccgggga ggcacaggtg gccccacca cccggaggag 400
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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<210> 510
<211> 273
<212> PRT
<213> Homo sapiens

<400> 510

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
140 145 150

Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 511
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 511
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<210> 512
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 512
ttttccactc ctgtcgggtt gg 22

<210> 513
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 513
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200
cccgtgggc cggtttatcg ggaggagatt gtcttcagg gctagcaatt 250
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300
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ggtagacagg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450
atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

	305		310		315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu					
	320		325		330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu					
	335		340		345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala					
	350		355		360
Glu Ala Glu Lys					

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
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 atcgt 255

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 517
 caacgtgatt tcaaagctgg gctc 24

<210> 518
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

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<212> PRT

<213> Homo sapiens

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Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
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Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
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Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
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Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
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Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly
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Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro
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Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val
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Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
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Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
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Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
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Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
230 235 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp
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Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys
260 265 270

Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val
275 280 285

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
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Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
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<212> DNA

<213> Homo sapiens

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<212> DNA

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Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro
50 55 60

Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly
65 70 75

Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp
80 85 90

Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu
95 100 105

Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp
110 115 120

Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe
125 130 135

Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu
140 145 150

Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro
155 160 165

Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly
170 175 180

Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala
185 190 195

Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala
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Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser
215 220 225

Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala
230 235 240

Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu
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Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met
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Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val
275 280 285

Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met
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Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu
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Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser
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Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser
335 340 345

Glu Leu Ile Asn Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr Leu
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Lys Lys Ser Cys Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn Thr
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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
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Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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aaataagaaa atttctcaagg aggacgagct cttgagttag acccaacaag 150
ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250
cctgatactg ctcaccgctg gcgctgggct gctggtgggc caagtctga 300
atctgcaggc gcggctccgg gtcctggaga tgtatttctt caatgacact 350
ctggcgggctg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400
tggaagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450
aactcacctg ggtccgcgtc agccatgagc acttgctgca gcgggtagac 500
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cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600
gcccgcgggg accacctgct gagaaggagg ccaagggggc tatgggacga 650
gatggagcaa caggccctc gggaccccaa ggcccaccgg gagtcaaggg 700
agaggcgggc ctccaaggac ccagggtgc tccagggaag caaggagcca 750
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ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850

~~gggtctccca ggaagcaaag gggacagggg catgaaagga gatgcagggg 900~~

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 gcgtctgacc cggaaaccct ttcacttctc tgctcccagag gtgtcctcgg 1700
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 tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614
 <211> 520
 <212> PRT
 <213> Homo Sapien

<400> 614
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 1 5 10 15
 Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
 20 25 30
 Ile Asn Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser
 35 40 45
 Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala
 50 55 60
 Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg
 65 70 75
 Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp
 80 85 90
 Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His
 95 100 105
 Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu
 110 115 120
 Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp
 125 130 135
 Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Ile Lys Gly Glu Gln
 140 145 150
 Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro
 155 160 165
 Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys
 170 175 180
 Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln

	185	190	195
Gly Pro Pro Gly	Val Lys Gly Glu Ala	Gly Leu Gln Gly Pro	Gln
	200	205	210
Gly Ala Pro Gly	Lys Gln Gly Ala Thr	Gly Thr Pro Gly Pro	Gln
	215	220	225
Gly Glu Lys Gly	Ser Lys Gly Asp Gly	Gly Leu Ile Gly Pro	Lys
	230	235	240
Gly Glu Thr Gly	Thr Lys Gly Glu Lys	Gly Asp Leu Gly Leu	Pro
	245	250	255
Gly Ser Lys Gly	Asp Arg Gly Met Lys	Gly Asp Ala Gly Val	Met
	260	265	270
Gly Pro Pro Gly	Ala Gln Gly Ser Lys	Gly Asp Phe Gly Arg	Pro
	275	280	285
Gly Pro Pro Gly	Leu Ala Gly Phe Pro	Gly Ala Lys Gly Asp	Gln
	290	295	300
Gly Gln Pro Gly	Leu Gln Gly Val Pro	Gly Pro Pro Gly Ala	Val
	305	310	315
Gly His Pro Gly	Ala Lys Gly Glu Pro	Gly Ser Ala Gly Ser	Pro
	320	325	330
Gly Arg Ala Gly	Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala	Thr
	335	340	345
Gly Leu Lys Gly	Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln	Gln
	350	355	360
Gly Arg Lys Gly	Glu Ser Gly Val Pro	Gly Pro Ala Gly Val	Lys
	365	370	375
Gly Glu Gln Gly	Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala	Pro
	380	385	390
Gly Gln Ala Gly	Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser	Ser
	395	400	405
Gly Glu Gln Gly	Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu	Asn
	410	415	420
Ser Val Ser Val	Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg	Ala
	425	430	435
Glu Val Tyr Tyr	Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp	Glu
	440	445	450
Trp Gln Asn Ser	Asp Ala Ile Val Phe	Cys Arg Met Leu Gly	Tyr
	455	460	465
Ser Lys Gly Arg	Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly	Gln

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
	485		490		495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
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 atttaagaag catcctctgc caagaccaaa aggaaagaag aaaaagggcc 150
 aaaagccaaa atgaaactga tggctactgt tttcaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgcctgcaa atcgctctc ttgctacaga 250
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 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtcaa 550
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 gttaaacaag tagtaataaa agttaattca atctaataaa aaaaaaa 647

<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
 1 5 10 15
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
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 accccgcogt ggtggttggg gggcgcgag tagagcagca gcacaggcgc 150
 gggccccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200
 cgaaaccgac tgggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250
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 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
 tttcagcttg caaagcaa atcaatccag tggaaagaat ttggcctgga 500
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 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650
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 aaggagtcac tctctactcc gacctgctg actactttgc tctgggggtg 900
 aagtcctatc cagacggttg gaatcttctt ggaggtggtg tccagcgtgg 950

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cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050
ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100
agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150
tcaaagtgcc ctacaatggt ggacctggct ttactggaaa cttttctaca 1200
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caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300
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agtggagcag ctgttggtca tgaaattgtg aggagctttg gaacactgaa 1400
aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctgggatg 1450
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acagaaattg cttccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150
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gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300
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aggcctgggg agaagtgaag agacagattt atgttcagc cttcacagtg 2400

caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450
 gaatccgtat tgaatttggtg tggtatgtca ctcagaaaga atcgtaatgg 2500
 gtatatgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550
 atatataa 2558

<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618
 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala
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 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
 20 25 30
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
 35 40 45
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
 50 55 60
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
 65 70 75
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 80 85 90
 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
 95 100 105
 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
 110 115 120
 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
 125 130 135
 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
 140 145 150
 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
 155 160 165
 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
 170 175 180
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
 185 190 195
 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
 200 205 210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu	485	490	495

Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	500	505	510
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	515	520	525
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	530	535	540
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	545	550	555
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	560	565	570
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	575	580	585
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	590	595	600
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	605	610	615
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp	620	625	630
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys	635	640	645
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val	650	655	660
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe	665	670	675
Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val	680	685	690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe	695	700	705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp	710	715	720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	725	730	735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala	740	745	750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccgta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tgggaaatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50